46875

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From: Jiang, Dong
Sent: Monday, July 16, 2001 4:11 PM
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Subject: SN09/488,728

Please search 1 to 322 of SEQ ID NO:2, and
1 to 320 of SEQ ID NO:4

-issued
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Dong Jiang (78243)
703-305-1345
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Access DB# 46815

SEARCH REQUEST FORM

Scientific and Technical Information Center

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Mail Box and Bldg/Room Location:_____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

****

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NA Sequence (#)_____
AA Sequence (#) 2
Structure (#) _____
Bibliographic _____
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Patent Family _____
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Vendors and cost where applicable

STN _____
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Questel/Orbit _____
Dr.Link _____
Lexis/Nexis _____
Sequence Systems AGS502
WWW/Internet _____
Other (specify)_____

PTO-1590 (1-2000)

Tue Jul 17 11:27:36 2001

us-09-488-728-4_copy_1_320.rspt

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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:20:41 ; Search time 38.21 Seconds
(without alignments)
1108.024 Million cell updates/sec

Title: US-09-488-728-4_COPY_1_320
Perfect score: 1764
Sequence: 1 MGAARSPPSAVPGPLLGLLL.....VSCPEMPDTPEPIPDYMPLW 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1764	100.0	866	4	O43844	O43844 homo sapien
2	1254	71.1	864	11	Q60943	Q60943 mus musculu
3	286	16.2	426	4	Q9NRL4	Q9nrl4 homo sapien
4	284	16.1	502	4	Q9NRM6	Q9nrm6 homo sapien
5	272.5	15.4	499	11	Q9JIP3	Q9jip3 mus musculu
6	220	12.5	288	4	Q9NRM5	Q9nrm5 homo sapien
7	166.5	9.4	218	11	Q9JIP2	Q9jip2 mus musculu
8	97.5	5.5	398	5	O61939	O61939 caenorhabdi
9	96.5	5.5	800	5	Q9U980	Q9u980 drosophila
10	96.5	5.5	800	5	Q9W4I2	Q9w4i2 drosophila
11	93	5.3	1204	4	Q9H0H0	Q9h0h0 homo sapien
12	93	5.3	1209	4	Q9ULD3	Q9uld3 homo sapien
13	92.5	5.2	1233	5	Q9VGY6	Q9vgy6 drosophila
14	92	5.2	509	11	Q9QWI5	Q9qwi5 rattus norv
15	92	5.2	593	10	Q9SJR7	Q9sjr7 arabidopsis
16	92	5.2	623	5	P90533	P90533 dictyosteli
17	90.5	5.1	260	7	Q06746	Q06746 xenopus lae
18	90.5	5.1	744	5	Q9GPJ1	Q9gpj1 drosophila
19	90.5	5.1	1870	14	Q9J5A0	Q9j5a0 fowlpox vir
20	90	5.1	509	11	P97710	P97710 rattus norv
21	89.5	5.1	418	11	O70426	O70426 rattus norv
22	89.5	5.1	471	11	Q9R1F9	Q9r1f9 mus musculu
23	88.5	5.0	1144	10	Q40392	Q40392 nicotiana g
24	88	5.0	679	10	Q9ZWD7	Q9zwd7 arabidopsis
25	88	5.0	4340	2	O30764	O30764 streptomyce
26	87.5	5.0	234	10	Q9SN88	Q9sn88 arabidopsis
27	87.5	5.0	397	11	O35325	O35325 mus musculu
28	87	4.9	635	5	P91092	P91092 caenorhabdi
29	87	4.9	1216	11	Q62884	Q62884 rattus norv
30	87	4.9	1341	5	Q9VIL0	Q9vil0 drosophila
31	87	4.9	1515	4	Q9NU48	Q9nu48 homo sapien
32	87	4.9	1522	4	Q9P2D6	Q9p2d6 homo sapien
33	86.5	4.9	249	14	Q9E8I9	Q9e8i9 human rotav
34	86.5	4.9	771	4	Q9HCN3	Q9hcn3 homo sapien
35	86	4.9	4578	13	O42181	O42181 fugu rubrip
36	85.5	4.8	397	11	O35118	O35118 mus musculu
37	84.5	4.8	323	2	Q9KXW9	Q9kxw9 streptomyce
38	84.5	4.8	397	11	O55243	O55243 mus musculu
39	84.5	4.8	1047	4	Q9HC39	Q9hc39 homo sapien
40	84.5	4.8	1047	4	Q9HBB9	Q9hbb9 homo sapien
41	84.5	4.8	1059	13	Q9DE49	Q9de49 brachydanio
42	84.5	4.8	1151	3	O13987	O13987 schizosacch
43	84.5	4.8	1442	4	Q92735	Q92735 homo sapien
44	84.5	4.8	1956	4	O43154	O43154 homo sapien
45	84	4.8	244	11	Q9ESA4	Q9esa4 rattus norv

ALIGNMENTS

RESULT 1
O43844
ID O43844 PRELIMINARY; PRT; 866 AA.
AC O43844;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE IL-17 RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98035683; PubMed=9367539;
RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,
RA VandenBos T., Zappone J., Painter S.L., Armitage R.J.;
RT "Molecular characterization of the human interleukin (IL)-17
RT receptor.";
RL Cytokine 9:794-800(1997).
DR EMBL; U58917; AAB99730.1; -.
SQ SEQUENCE 866 AA; 96121 MW; 88AF626A83F3FF70 CRC64;

Query Match 100.0%; Score 1764; DB 4; Length 866;
Best Local Similarity 100.0%; Pred. No. 1.2e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy    241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy    301 VSCPEMPDTPEPIPDYMPLW 320
          ||||||||||||||||||||
Db    301 VSCPEMPDTPEPIPDYMPLW 320


RESULT   2
Q60943
ID   Q60943       PRELIMINARY;      PRT;   864 AA.
AC   Q60943;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   INTERLEUKIN 17 RECEPTOR.
GN   IL17R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=THYMOMA EL4;
RX   MEDLINE=96111968; PubMed=8777726;
RA   Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,
RA   Comeau M.R., Cohen J.I., Spriggs M.K.;
RT   "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a
RT   novel cytokine receptor.";
RL   Immunity 3:811-821(1995).
DR   EMBL; U31993; AAC52357.1; -.
DR   MGD; MGI:107399; Il17r.
SQ   SEQUENCE   864 AA;  97807 MW;  343FD51AA687DA31 CRC64;

  Query Match             71.1%;  Score 1254;  DB 11;  Length 864;
  Best Local Similarity   71.4%;  Pred. No. 1.4e-114;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy      1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
          |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db      1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60

Qy     61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
          |||||:|||||||:: | |  : || |:| || |:|||||||||||||||||||||||||
Db     61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120

Qy    121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
          |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||:||
Db    121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180

Qy    181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
          ||||| ::||:|| |:|||||||||||||:   ||| |||||||| ||:|| ||
Db    181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240

Qy    241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
          ||||||: :  | ||| ||||||:||| ||      || | ||:|||||||||||||: |
Db    241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300

Qy    301 VSCPEMPDT--PEPIPDYMPLW 320
          | || : :|  |:|: ||:|||
Db    301 VPCPVISNTTVPKPVADYIPLW 322


RESULT   3
Q9NRL4
ID   Q9NRL4       PRELIMINARY;      PRT;   426 AA.
AC   Q9NRL4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   IL-17B RECEPTOR.
GN   IL17BR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20317118; PubMed=10749887;
RA   Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
RA   Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,
RA   Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
RA   Carrell J.A., Ebner R.;
RT   "A novel cytokine receptor-ligand pair. Identification, molecular
RT   characterization, and in vivo immunomodulatory activity.";
RL   J. Biol. Chem. 275:19167-19176(2000).
DR   EMBL; AF212365; AAF78776.1; -.
KW   Receptor.
SQ   SEQUENCE   426 AA;  47137 MW;  D5B820CCEFC12E27 CRC64;

  Query Match             16.2%;  Score 286;  DB 4;  Length 426;
  Best Local Similarity   27.2%;  Pred. No. 6.4e-20;
  Matches   83;  Conservative   48;  Mismatches  142;  Indels   32;  Gaps    8;

Qy     16 LGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSPKD 75
          : |:|| |  |                |: |  :| : |   : |     |:   :| |   :|
Db      1 MSLVLLSLAALC----------RSAVPREPTVQC--GSETGPSPEWMLQHDLIPGDLRD 47

Qy     76 LQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL-QLNTNERLCVRFE---- 130
          |:::         ||   : :: | |: ||||  |:  :: |  : |     |||
Db     48 LRVEPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEA 107

Qy    131 FLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARM 190
          | :: |    :| |::  | |: :  | :  |::|    : |    | ||  | |   |
Db    108 FQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIM 167

Qy    191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH 250
          |    |: :||||||||||          : |:||      |  |:          ||
Db    168 KYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI-------QHSTIIGFS 220

Qy    251 HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT-VSCPEMPDT 309
          :  |  ::  : | |      : :|      ||: |:| :| :||:||  | | ||:   |
Db    221 QVFEPHQKKQTRASVVIPVTGDSEGA---TVQLTPYFPTCGSDCIRHKGTVVLCPQ---T 274

Qy    310 PEPIP 314
          | |
Db    275 GVPFP 279


RESULT   4
Q9NRM6
ID   Q9NRM6       PRELIMINARY;      PRT;   502 AA.
AC   Q9NRM6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE   IL-17 RECEPTOR HOMOLOG PRECURSOR.
GN   EVI27.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20273223; PubMed=10815801;
RA   Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
RA   Shaughnessy J.D. Jr.;
RT   "Evi27 encodes a novel membrane protein with homology to the IL17
RT   receptor.";
RL   Oncogene 19:2098-2109(2000).
DR   EMBL; AF208110; AAF86051.1; -.
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KW   Signal; Receptor.
FT   SIGNAL        1     13       POTENTIAL.
FT   CHAIN        14    502       IL-17 RECEPTOR HOMOLOG.
SQ   SEQUENCE   502 AA;  55918 MW;  9C84A63EC123FF17 CRC64;

  Query Match           16.1%;  Score 284;  DB 4;  Length 502;
  Best Local Similarity 26.9%;  Pred. No. 1.2e-19;
  Matches   82;  Conservative   49;  Mismatches  142;  Indels   32;  Gaps    8;

Qy      16 LGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSPKD 75
           : |:|: | |                |: |  :| : |   : |     |:  :| |   :|
Db       1 MSLVLISLAALC----------RSAVPREPTVQC--GSETGPSPEWMLQHDLIPGDLRD 47

Qy      76 LQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL-QLNTNERLCVRFE---- 130
           |:::          ||   : :: | |: |||| |:  :: |  : |.    |||
Db      48 LRVEPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEA 107

Qy     131 FLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARM 190
           | :: |    :| |:: | |: :  | :  |::|    : |    | || | |     |
Db     108 FQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIM 167

Qy     191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH 250
           |    |: :|||||||||          : |:||     |  |:        ||
Db     168 KYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI-------QHSTIIGFS 220

Qy     251 HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT-VSCPEMPDT 309
           :  | ::  : | |      : :|     ||: |:| :| :||:||  | | ||:   |
Db     221 QVFEPHQKKQTRASVVIPVTGDSEGA---TVQLTPYFPTCGSDCIRHKGTVVLCPQ---T 274

Qy     310 PEPIP 314
           | |
Db     275 GVPFP 279


RESULT   5
Q9JIP3
ID   Q9JIP3       PRELIMINARY;      PRT;   499 AA.
AC   Q9JIP3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   IL-17 RECEPTOR HOMOLOG PRECURSOR.
GN   EVI27.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20273223; PubMed=10815801;
RA   Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
RA   Shaughnessy J.D. Jr.;
RT   "Evi27 encodes a novel membrane protein with homology to the IL17
RT   receptor.";
RL   Oncogene 19:2098-2109(2000).
DR   EMBL; AF208108; AAF86049.1; -.
KW   Signal; Receptor.
FT   SIGNAL        1      8       POTENTIAL.
FT   CHAIN         9    499       IL-17 RECEPTOR HOMOLOG.
SQ   SEQUENCE   499 AA;  55617 MW;  C66440430E3C31F3 CRC64;

  Query Match           15.4%;  Score 272.5;  DB 11;  Length 499;
  Best Local Similarity 27.6%;  Pred. No. 1.6e-18;
  Matches   89;  Conservative   45;  Mismatches  137;  Indels   51;  Gaps   11;

Qy      19 LLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSPKDLQI 78
           :||:| :||   ||     |: :  :| : |   : |     |:    |||   :|||:
Db       1 MLLVLLILA---ASC-----RSALPREPTIQC--GSETGPSPEWMVQHTLTPGDLRDLQV 50

Qy      79 QLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL-QLNTNERLCVRFE----FLS 133
           :|       :   : :| | |: |||| |:  :: |  : | |   |||       | |
Db      51 ELVKTSVAAEEFSILMNISWILRADASIRLLKATKICVSGKNNMNSYSCVRCNYTEAFQS 110

Qy     134 KLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVT 193
           : |    :| |:: | |:     | :: |::|    : |     | ||  | | :  ||
Db     111 QTRPSGGKWTFSYVGFPVELSTLYLISAHNIPNANMNEDSPSLSVNFTSPGCLNHVMKYK 170

Qy     194 TPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILL-----TSFPHMENHSCFEH 248
           |  :|||||||:||          : |:||     | ||:       |  :  :
Db     171 KQCTEAGSLWDPDITACKKNEKMVEVNFTTNPLGNRYTILIQRDTTLGFSRVLENKLMRT 230

Qy     249 MHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT-VSCPEMP 307
             ||    |                |     ||: |:  :| |||:|   | | | |
Db     231 SVAIPVTEESE----------GAV---VQLTPYLHTCGNDCIRREGTVVLCSE-- 270

Qy     308 DTPEPIP---------DYMPLW 320
           |  |||          ::||:
Db     271 -TSAPIPPDDNRRMLGGWLPLF 291


RESULT   6
Q9NRM5
ID   Q9NRM5       PRELIMINARY;      PRT;   288 AA.
AC   Q9NRM5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   TRUNCATED IL-17 RECEPTOR HOMOLOG PRECURSOR.
GN   EVI27.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20273223; PubMed=10815801;
RA   Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
RA   Shaughnessy J.D. Jr.;
RT   "Evi27 encodes a novel membrane protein with homology to the IL17
RT   receptor.";
RL   Oncogene 19:2098-2109(2000).
DR   EMBL; AF208111; AAF86052.1; -.
KW   Signal; Receptor.
FT   SIGNAL        1     13       POTENTIAL.
FT   CHAIN        14    288       TRUNCATED IL-17 RECEPTOR HOMOLOG.
SQ   SEQUENCE   288 AA;  31773 MW;  CD8EB2C0C235FBFB CRC64;

  Query Match           12.5%;  Score 220;  DB 4;  Length 288;
  Best Local Similarity 26.8%;  Pred. No. 1.3e-13;
  Matches   60;  Conservative   37;  Mismatches  109;  Indels   18;  Gaps    4;

Qy      16 LGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSPKD 75
           : |:|: | |                |: |  :| : |   : |     |:  :| |   :|
Db       1 MSLVLISLAALC----------RSAVPREPTVQC--GSETGPSPEWMLQHDLIPGDLRD 47

Qy      76 LQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL-QLNTNERLCVRFE---- 130
           |:::          ||   : :: | |: |||| |:  :: |  : |.    |||
Db      48 LRVEPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEA 107

Qy     131 FLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARM 190
           | :: |    :| |:: | |: :  | :  |::|    : |    | || | |     |
Db     108 FQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIM 167

Qy     191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILL 234
           |    |: :|||||||||          : |:||     |  |:
Db     168 KYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI 211


RESULT   7
Q9JIP2
ID   Q9JIP2       PRELIMINARY;      PRT;   218 AA.
AC   Q9JIP2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
```

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DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   IL-17 RECEPTOR HOMOLOG SHORT ISOFORM PRECURSOR.
GN   EVI27.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20273223; PubMed=10815801;
RA   Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
RA   Shaughnessy J.D. Jr.;
RT   "Evi27 encodes a novel membrane protein with homology to the IL17
RT   receptor.";
RL   Oncogene 19:2098-2109(2000).
DR   EMBL; AF208109; AAF86050.1; -.
DR   InterPro; IPR002259; -.
DR   ProDom; PD005103; -; 1.
KW   Signal; Receptor.
FT   SIGNAL       1      8       POTENTIAL.
FT   CHAIN        9    218       IL-17 RECEPTOR HOMOLOG SHORT ISOFORM.
SQ   SEQUENCE   218 AA;  23855 MW;  E17C154C824E1F0B CRC64;

  Query Match             9.4%;  Score 166.5;  DB 11;  Length 218;
  Best Local Similarity  28.2%;  Pred. No. 1.6e-08;
  Matches   51;  Conservative   32;  Mismatches   83;  Indels   15;  Gaps    5;

Qy      19 LLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSPKDLQI 78
           :||:| :||   ||      |: :  :| : |   : |      |:   |||   :|||:
Db       1 MLLVLLILA---ASC-----RSALPREPTIQC--GSETGPSPEWMVQHTLTPGDLRDLQV 50

Qy      79 QLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL-QLNTNERLCVRFE----FLS 133
           :|      :   : :| | |: |||| |:  :: |  : | |   |||       | |
Db      51 ELVKTSVAAEEFSILMNISWILRADASIRLLKATKICVSGKNNMNSYSCVRCNYTEAFQS 110

Qy     134 KLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVT 193
           : |    :| |::  | |:    | :: |::|    : |    | ||  | |     :||
Db     111 QTRPSGGKWTFSYVGFPVELSTLYLISAHNIPNANMNEDSPSLSVNFTSPGCTRENTEVT 170

Qy     194 T 194
           :
Db     171 S 171


RESULT   8
O61939
ID   O61939      PRELIMINARY;      PRT;   398 AA.
AC   O61939;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   T24A6.8 PROTEIN.
GN   T24A6.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Taich A., Gattung S., Le T.T.;
RT   "The sequence of C. elegans cosmid T24A6.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC   -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR   EMBL; AF068713; AAC17795.2; -.
DR   HSSP; P10828; 2NLL.
DR   InterPro; IPR000536; -.
DR   InterPro; IPR001628; -.
DR   Pfam; PF00104; hormone_rec; 2.
DR   Pfam; PF00105; zf-C4; 2.
DR   PRINTS; PR00047; STROIDFINGER.
DR   SMART; SM00430; HOLI; 1.
DR   SMART; SM00399; ZnF_C4; 1.
KW   DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW   Zinc-finger.
SQ   SEQUENCE   398 AA;  46295 MW;  DD051AE817F8A437 CRC64;

  Query Match             5.5%;  Score 97.5;  DB 5;  Length 398;
  Best Local Similarity  20.5%;  Pred. No. 0.19;
  Matches   66;  Conservative   38;  Mismatches   89;  Indels  129;  Gaps   16;

Qy      39 RALVCSQP--GLNCTV-------------------KNSTCLDDSWIHPRN--------- 67
           : :|| :|  | :| |                   | ||  |   :  ||
Db      33 KCMVCVRPAHGYHCDVATCKGCKTFFRRMCLLRGEIKCSTSGDCYDLEKRNSPLLRCRPC 92

Qy      68 ------LTPSSPKDLQI---------QLHFAHTQ-QGDLFPVAHIEWTLQTDASILY--- 108
                |   :|| | |          |:||   | || :  ::|:|   :  :  |
Db      93 RFKRCLLVGMNPKALIIDGSNILGEKQVHFNEQQIQGTIDVLSHLEAKTEQFSKCAYNPD 152

Qy     109 -----LEGAELSVLQLNTNER--------LCVRFEFLSKLRH--------HHRRWRF--- 144
               |:   ||  :|: :::         ||  :||  :: |         | ::|||
Db     153 WTNIRLKDLILSPSKLSMSDKVGTFPDWPLCPNYEFPDQIVHRDIQSFSPHRKQWRFSNL 212

Qy     145 --------TFSHF-------------VVDPDQEYEVTVHHLPKPI-----PDG------ 171
                  |||                ||     | : |          |||
Db     213 MTAVEYTKTFSFFHDLSFQDQINLLKHVVIGLANFNTTYYTLKNKFDDLRQPDGTQRPGV 272

Qy     172 -DPNH--------QSKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFT 222
            :|::          |   :   |   :|:  |                |  |  |  |
Db     273 NEPHYCAHTVPFGPMKRIKIQFNEFLLLKILFVC---------NPAVPNLSKH---AQFV 320

Qy     223 LWNESTHYQILLTSFPHMENHS 244
           :  |  ||  :|  :  ::|:|
Db     321 IEKERHHYSNILLKY-CLQNYS 341


RESULT   9
Q9U980
ID   Q9U980      PRELIMINARY;      PRT;   800 AA.
AC   Q9U980;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   CAP BINDING PROTEIN 80.
GN   CBP80 OR EG:84H4.3 OR CG7035.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OREGON R; TISSUE=IMAGINAL DISC;
RA   Lewis J.D.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ238970; CAB53186.1; -.
DR   FlyBase; FBgn0022942; Cbp80.
SQ   SEQUENCE   800 AA;  93070 MW;  7C9E7948ABD876B6 CRC64;
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 Query Match             5.5%;  Score 96.5;  DB 5;  Length 800;
 Best Local Similarity   21.5%;  Pred. No. 0.51;
 Matches   56;  Conservative   31;  Mismatches   93;  Indels   81;  Gaps   12;

Qy      48 LNCTVKNSTCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASIL 107
           :|| | ::| |                 ||:           | |   :| :    | |
Db     138 VNCHVISATSL----------------LQLLDTMIDVSNEDTVPQVRRDWFVFAVLSTL 180

Qy     108 YLEGAELSVLQLNTNERLCVRFE-FLSK--LRHHH--RRWRFTFSHFVVDPDQEY----- 157
           | :|   : :  | | :| | :|:|   :||:  | |     |   | :||
Db     181 PWVGRDLYEKKESALESLLLRIEVYLNKRSKKHHNALRVWSSDAPH----PQEEYLDCLW 236

Qy     158 ---------------------------EVTVHHLPKPIPDGDPNHQSKNFLVPDCEHAR 189
                                       |   |:||  :|   |:| :  : :|   : |
Db     237 AQIRKLRQDNWAEKHIPRPYLVFDSILCEALQHNLPTIVP--PPHHDNFEYPMPWVVY-R 293

Qy     190 MKVTTPCMSSGSLWDPNI----TVE--TLEAHQLRVSFTLWNESTHYQILLTSFPHMEN- 242
           |   | |        ||:    ::|   :| |   :|  :|       | |||:
Db     294 MFDYTDCPDG-----PNLPGAHSIERFLIEEHLHHIIETYHHERKDCAAQLLSFPYKHKI 348

Qy     243 -------HSCFEHMHHIPAPR 256
                  |  : |:| ||
Db     349 PLEYCIVEVVFAELFHMPTPR 369
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RESULT  10
Q9W4I2
ID   Q9W4I2      PRELIMINARY;      PRT;   800 AA.
AC   Q9W4I2; O77276;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   CBP80 PROTEIN (EG:84H4.3 PROTEIN).
GN   CBP80 OR EG:84H4.3 OR CG7035.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE OF 1-348 FROM N.A.
RA   Ferraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.;
RT   "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 1-348 FROM N.A.
RA   Benos P.;
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003431; AAF45970.1; -.
DR   EMBL; AL031766; CAA21136.1; -.
DR   FlyBase; FBgn0022942; Cbp80.
SQ   SEQUENCE   800 AA;  93226 MW;  4D90C157E9A33B9B CRC64;
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 Query Match             5.5%;  Score 96.5;  DB 5;  Length 800;
 Best Local Similarity   21.5%;  Pred. No. 0.51;
 Matches   56;  Conservative   31;  Mismatches   93;  Indels   81;  Gaps   12;

Qy      48 LNCTVKNSTCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASIL 107
           :|| | ::| |                 ||:           | |   :| :    | |
Db     138 VNCHVISATSL----------------LQLLDTMIDVSNEDTVPQVRRDWFVFAVLSTL 180

Qy     108 YLEGAELSVLQLNTNERLCVRFE-FLSK--LRHHH--RRWRFTFSHFVVDPDQEY----- 157
           | :|   : :  | | :| | :|:|   :||:  | |     |   | :||
Db     181 PWVGRDLYEKKESALESLLLRIEVYLNKRSKKHHNALRVWSSDAPH----PQEEYLDCLW 236

Qy     158 ---------------------------EVTVHHLPKPIPDGDPNHQSKNFLVPDCEHAR 189
                                       |   |:||  :|   |:| :  : :|   : |
Db     237 AQIRKLRQDNWAEKHIPRPYLVFDSILCEALQHNLPTIVP--PPHHDNFEYPMPWVVY-R 293

Qy     190 MKVTTPCMSSGSLWDPNI----TVE--TLEAHQLRVSFTLWNESTHYQILLTSFPHMEN- 242
           |   | |        ||:    ::|   :| |   :|  :|       | |||:
Db     294 MFDYTDCPDG-----PNLPGAHSIERFLIEEHLHHIIETYHHERKDCAAQLLSFPYKHKI 348

Qy     243 -------HSCFEHMHHIPAPR 256
                  |  : |:| ||
Db     349 PLEYCIVEVVFAELFHMPTPR 369
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RESULT  11
Q9H0H0
ID   Q9H0H0      PRELIMINARY;      PRT;  1204 AA.
AC   Q9H0H0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   HYPOTHETICAL 134.3 KDA PROTEIN.
GN   DKFZP434H1220.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RA   Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL136800; CAB66734.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   1204 AA;  134345 MW;  50B87F6FFF2A1088 CRC64;
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 Query Match             5.3%;  Score 93;  DB 4;  Length 1204;
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  Best Local Similarity   22.3%;  Pred. No. 1.8;
  Matches   88;  Conservative   36;  Mismatches  112;  Indels  158;  Gaps   23;

Qy      29 GGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPS----------------S 72
           ||     ||  | |  : | |          |: | ||    :| :                 |
Db     704 GGLHSALL--RLLATNYPHL--------CIVDDWICEEEITGTDALLRRMLLTNNAKNHS 753

Qy      73 PKDL----------------QIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL 117
           || |                ||  |        :| | | :   | :: | |    |    :|
Db     754 PKQLQEAFSAVPVNHTQVMQIIEHLTLLSASELIPYAEV---LTSNMSQLLNSGVPRRIL 810

Qy     118 Q--------LNT--NERLCV--------RFEFLSKLRHHHRRWRFTFSHFVVDP------ 153
           |        |||    || |          :|:       |: ::| :  ::||
Db     811 QTVNKLWMVLNTVMPRRLWVMTVNALQPSIKFV-------RQQKYTQNDLMIDPLIVLRC 863

Qy     154 DQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEH--ARMKVT---TPCMSS-----GSLW 203
           ||     ||  | |: |    |    :|:    :  | :| |    |  ::     |
Db     864 DQR----VHRCP-PLMD-ITLHMLNGYLLASKAYLSAHLKETEQDRPSQNNTIGLVGQTD 917

Qy     204 DPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAPRPEEFHQR 263
           | :| |     :|: :     :|   ||||                 |  |  ||
Db     918 APEVTRE-----ELKNALLAAQDSAAVQILL---------------EICLPTEEEKANG 956

Qy     264 SNVTLTLRNL----------KG---------CCRHQVQIQPFFSSCLNDCLRHSATVS-- 302
           |    |||:           ||         |   :||       ||  || |   ::
Db     957 VNPDSLLRNVQSVITTSAPNKGMEEGEDNLLCNLREVQ-------CLICCLLHQMYIADP 1009

Qy     303 -----------CPEMPDTPEPIP------DYMP 318
                     |  :| |   ||      |::|
Db    1010 NIAKLVHFQGYPCELLPLTVAGIPSMHICLDFIP 1043


RESULT  12
Q9ULD3
ID   Q9ULD3      PRELIMINARY;      PRT;  1209 AA.
AC   Q9ULD3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   KIAA1287 PROTEIN (FRAGMENT).
GN   KIAA1287.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=20039619; PubMed=10574462;
RA   Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XV.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 6:337-345(1999).
DR   EMBL; AB033113; BAA86601.1; -.
FT   NON_TER      1       1
SQ   SEQUENCE   1209 AA;  134941 MW;  BF44BD99F71A37B9 CRC64;


  Query Match             5.3%;  Score 93;  DB 4;  Length 1209;
  Best Local Similarity   22.3%;  Pred. No. 1.8;
  Matches   88;  Conservative   36;  Mismatches  112;  Indels  158;  Gaps   23;

Qy      29 GGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPS----------------S 72
           ||     ||  | |  : | |          |: | ||    :| :                 |
Db     709 GGLHSALL--RLLATNYPHL--------CIVDDWICEEEITGTDALLRRMLLTNNAKNHS 758

Qy      73 PKDL----------------QIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL 117
           || |                ||  |        :| | | :   | :: | |    |    :|
Db     759 PKQLQEAFSAVPVNHTQVMQIIEHLTLLSASELIPYAEV---LTSNMSQLLNSGVPRRIL 815

Qy     118 Q--------LNT--NERLCV--------RFEFLSKLRHHHRRWRFTFSHFVVDP------ 153
           |        |||    || |          :|:       |: ::| :  ::||
Db     816 QTVNKLWMVLNTVMPRRLWVMTVNALQPSIKFV-------RQQKYTQNDLMIDPLIVLRC 868

Qy     154 DQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEH--ARMKVT---TPCMSS-----GSLW 203
           ||     ||  | |: |    |    :|:    :  | :| |    |  ::     |
Db     869 DQR----VHRCP-PLMD-ITLHMLNGYLLASKAYLSAHLKETEQDRPSQNNTIGLVGQTD 922

Qy     204 DPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAPRPEEFHQR 263
           | :| |     :|: :     :|   ||||                 |  |  ||
Db     923 APEVTRE-----ELKNALLAAQDSAAVQILL---------------EICLPTEEEKANG 961

Qy     264 SNVTLTLRNL----------KG---------CCRHQVQIQPFFSSCLNDCLRHSATVS-- 302
           |    |||:           ||         |   :||       ||  || |   ::
Db     962 VNPDSLLRNVQSVITTSAPNKGMEEGEDNLLCNLREVQ-------CLICCLLHQMYIADP 1014

Qy     303 -----------CPEMPDTPEPIP------DYMP 318
                     |  :| |   ||      |::|
Db    1015 NIAKLVHFQGYPCELLPLTVAGIPSMHICLDFIP 1048


RESULT  13
Q9VGY6
ID   Q9VGY6      PRELIMINARY;      PRT;  1233 AA.
AC   Q9VGY6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   CG14682 PROTEIN.
GN   CG14682.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003688; AAF54536.1; -.
DR   FlyBase; FBgn0037821; CG14682.
DR   InterPro; IPR002903; -.
DR   ProDom; PD004685; -; 1.
SQ   SEQUENCE   1233 AA;  135198 MW;  5E4E1DB29E45CB30 CRC64;


  Query Match             5.2%;  Score 92.5;  DB 5;  Length 1233;
  Best Local Similarity   26.0%;  Pred. No. 2;
  Matches   50;  Conservative   20;  Mismatches   79;  Indels   43;  Gaps   11;

Qy     153 PDQEYEVT-VHHLPKPIPDG----------------DPNHQSKNFLVPDCEHARMKVTT 194
           |   :|:|    : | | ||              .      :||| ::|  :|:  | :  ||
Db     527 PKLSFEITKSSEITKLISDGIRAAEALEESLLRNPNLNPNHPNQN-PIPN-PHQKPNVTP 584

Qy     195 PCMSSGSLWDPNITVETLEAHQLRV----------SFTLWNESTHYQILLTSFPHMENHS 244
             :||     | | :    || |           | || : :    ||    ||: :|
Db     585 TEISS----RPEILLGETHAHTLNASPSASAYPSPSATLPSANLKLPILAAG-PHLIHHP 639

Qy     245 CFEH-MHHIP--APRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSATV 301
           | :|| |  || |       |:|    ||    :  : :  |      |  | |   |
Db     640 PHLHRLHHQPQHAPHPHVHLHHHNLT---ANLPALAQKTIGLSEFLRPPQNAPLFH--PV 694

Qy     302 SCPEMPDTPEPI 313
             |    | ||
Db     695 KLPGRRPFPAPI 706


RESULT  14
Q9QWI5
ID   Q9QWI5      PRELIMINARY;      PRT;   509 AA.
AC   Q9QWI5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   MACROPHAGE MEMBRANE PROTEIN MFP150.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISHER 344;
RX   MEDLINE=98449911; PubMed=9774638;
RA   Saginario C., Sterling H., Beckers C., Kobayashi R., Solimena M.,
RA   Ullu E., Vignery A.;
RT   "MFR, a putative receptor mediating the fusion of macrophages.";
RL   Mol. Cell. Biol. 18:6213-6223(1998).
DR   EMBL; U62328; AAC68478.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003600; -.
DR   Pfam; PF00047; ig; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE   509 AA;  55655 MW;  44D812EFDEBCDEEF CRC64;


  Query Match             5.2%;  Score 92;  DB 11;  Length 509;
  Best Local Similarity   22.6%;  Pred. No. 0.86;
  Matches   79;  Conservative   42;  Mismatches   97;  Indels  132;  Gaps   22;

Qy       7 PPSAVP---GPLLGLLLLLLGVLAPG--GASLRLLDHRALVCSQPG----LNCTVKNSTC 57
           |    |   ||||  |||    :  |  |  |::     |    |   .|||||
Db       3 PAGPAPGRLGPLLFCLLLSASCICAGASGKELKVTQADKSVSVAAGDSATLNCTVS---- 58

Qy      58 LDDSWIHPRNLTPSSPKDLQIQLHFAHTQQ---------GDLFPVAHIEWTLQTDASILY 108
                  :|||  |    |:      |          |: ||      |  :||:
Db      59 ---------SLTPVGP----IKWFKGEGQNRSPIYSFIGGEHFP----RITNVSDAT--K 99

Qy     109 LEGAELSVLQLNTNER-----LCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYE----V 159
                 : |:   |          ||:|:                    :|:|| | :
```

```
Db     100 RNNMDFSICISNVTPEDAGTYYCVKFQ----------------KGIVEPDTEIKSGGGT 142

Qy     160 TVHHLPKPI------PD--GDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDP-NITVE 210
           |:: | ||        ||  | |  |: ||              | | |  : | |||::
Db     143 TLYVLAKPSSPEVSGPDSRGSPG-QTVNF-------------TCKSYG--FSPRNITLK 185

Qy     211 TLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAP-----RPEEFHQR-- 263
             |:  :         | :| :  ::|  ::          ::| :      ||: | |
Db     186 WLKNGK---------ELSHLETTISSKSNVS--------YNISSTVSVKLSPEDIHSRVI 228

Qy     264 ---SNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTP 310
               ::|||  | | |             ::  :: :| | |:   : | ||
Db     229 CEVAHVTLEGRPLNG-----------TANFSNIIRVSPTLKITQQPLTP 266


RESULT  15
Q9SJR7
ID   Q9SJR7      PRELIMINARY;      PRT;   593 AA.
AC   Q9SJR7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   AT2G36370 PROTEIN.
GN   AT2G36370.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC   Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA   Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA   Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA   Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA   Salzberg S.L., Fraser C.M., Venter J.C.;
RT   "Sequence and analysis of chromosome II of Arabidopsis thaliana.";
RL   Nature 402:761-768(1999).
DR   EMBL; AC006919; AAF18663.1; -.
DR   InterPro; IPR003592; -.
DR   SMART; SM00370; LRR; 1.
SQ   SEQUENCE   593 AA;  66690 MW;  4F12339EB86351D5 CRC64;


  Query Match             5.2%;  Score 92;  DB 10;  Length 593;
  Best Local Similarity   22.6%;  Pred. No. 1;
  Matches   67;  Conservative   33;  Mismatches  101;  Indels   96;  Gaps   15;

Qy      55 STCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDAS-ILYLEGAE 113
           |||| ||      ||   | |::::|                          |: | || | |
Db     182 STCLVDS------LTDGPPTDVRVRL--------------------TEYSEILDLSGCP 214

Qy     114 LSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDP--DQEYEVTVHHLPKPIPDG 171
               |||    |       |       : ||| :   |: :|  |: ::  : |   ||
Db     215 ----QLNEASLL---LSILPNSYFANLRWRKSLESFLKNPDDDERHQEQISHRTLPILSF 267

Qy     172 DPNHQSKNFLVPDCEHARMKVTTPCMSSG--------SLWDPNITVETLEAHQLRVSFTL 223
           :     |   :  |:    ||   | |          : :  || | ||   :| ::|
Db     268 E---SVKEIDISKCQRLDYKVVIKCFSKSFPSLRKLRAAYLLNIKVSTL--LELLLNFRE 322

Qy     224 WNE--------------STHY--QILLTSF---------------PHMENHSCFEHMH 250
           |                | |  |:  |||                  ||: :|   ::
Db     323 LTEVDLTVDVSPIIPVQASVFYSGQVCYTSFSENSILALCATISMTNEHMDINSVASNLQ 382

Qy     251 HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMP 307
           :  .: |   : | : |   :             |   | || |  : | :| | | |
Db     383 TLHMSKCEGISETSLLNLITHS----------QKMKSLCLRD-TKVSDSVLC-EFP 426
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Search completed: July 17, 2001, 11:20:43
Job time: 162 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:21:04 ; Search time 16.71 Seconds
(without alignments)
656.000 Million cell updates/sec

Title: US-09-488-728-4_COPY_1_320
Perfect score: 1764
Sequence: 1 MGAARSPPSAVPGPLLGLLL.....VSCPEMPDTPEPIPDYMPLW 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91.5	5.2	184	1	YC17_DROME	Q9vh95 drosophila
2	88.5	5.0	249	1	VS09_ROTGA	P18570 rotavirus (
3	88.5	5.0	1402	1	SALM_DROVI	P39806 drosophila
4	88	5.0	1210	1	EGFR_HUMAN	P00533 homo sapien
5	87.5	5.0	1714	1	SYEP_DROME	P28668 drosophila
6	86	4.9	439	1	XYLA_HAEIN	P44398 haemophilus
7	86	4.9	603	1	DOPO_HUMAN	P09172 homo sapien
8	85	4.8	607	1	KAIB_SCHPO	Q09898 schizosacch
9	84.5	4.8	1058	1	GEM4_HUMAN	P57678 homo sapien
10	83	4.7	191	1	INF_ANAPL	P51526 anas platyr
11	83	4.7	275	1	RPB3_MOUSE	P97760 mus musculu
12	83	4.7	740	1	PURL_LACCA	P35852 lactobacill
13	81.5	4.6	416	1	LMP1_HUMAN	P11279 homo sapien
14	81.5	4.6	558	1	Y653_HUMAN	O75144 homo sapien
15	81	4.6	275	1	RPB3_HUMAN	P19387 homo sapien
16	81	4.6	397	1	TBXT_CHICK	P79778 gallus gall
17	81	4.6	808	1	POLG_HPAVG	Q02381 hepatitis a
18	80.5	4.6	1164	1	DP3A_VIBCH	P52022 vibrio chol
19	80.5	4.6	1197	1	EVGS_ECOLI	P30855 escherichia
20	79.5	4.5	4753	1	LRP_CAEEL	Q04833 caenorhabdi
21	79	4.5	967	1	ATS1_RAT	Q9wuq1 rattus norv
22	78.5	4.5	1213	1	T2D2_DROME	Q24325 drosophila
23	78	4.4	352	1	AMBP_BOVIN	P00978 bos taurus
24	78	4.4	2242	1	PYR1_SQUAC	Q91437 squalus aca
25	77.5	4.4	272	1	E2F6_MOUSE	O54917 mus musculu
26	77.5	4.4	337	1	INGS_HUMAN	P38484 homo sapien
27	77.5	4.4	410	1	LMP2_HUMAN	P13473 homo sapien
28	77.5	4.4	587	1	FOLC_HUMAN	Q05932 homo sapien
29	77.5	4.4	843	1	CO7_HUMAN	P10643 homo sapien
30	77.5	4.4	1018	1	HIRA_CHICK	P79987 gallus gall
31	77	4.4	165	1	FUR_SYNY3	P74739 synechocyst
32	77	4.4	459	1	IL7R_HUMAN	P16871 homo sapien
33	77	4.4	484	1	CATA_CANAL	O13289 candida alb
34	77	4.4	903	1	AGLU_SPIOL	O04893 spinacia ol
35	77	4.4	961	1	ACON_MYCAV	O08451 mycobacteri
36	77	4.4	1015	1	HIRA_MOUSE	Q61666 mus musculu
37	77	4.4	1210	1	EGFR_MOUSE	Q01279 mus musculu
38	77	4.4	1587	1	SUR2_CAEEL	Q10669 caenorhabdi
39	76.5	4.3	432	1	BRAC_XENLA	P24781 xenopus lae
40	76.5	4.3	604	1	VGLE_SVVD	Q04548 simian vari
41	76.5	4.3	2255	1	RRPL_SV5	Q88434 simian viru
42	76.5	4.3	2255	1	RRPL_SV5WR	Q03396 simian viru
43	76	4.3	484	1	CATA_CANTR	P07820 candida tro
44	76	4.3	644	1	YEN9_YEAST	P40032 saccharomyc
45	76	4.3	879	1	DPOL_WHV1	P03160 woodchuck h

ALIGNMENTS

RESULT 1
YC17_DROME
ID YC17_DROME STANDARD; PRT; 184 AA.
AC Q9VH95;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN CG16817.
GN CG16817.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).

```
CC   -!- SIMILARITY: BELONGS TO THE P23 / WOS2 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; AE003683; AAF54424.1; -.
DR   FlyBase; FBgn0037728; CG16817.
KW   Hypothetical protein.
FT   DOMAIN      145    184       ASP/GLU-RICH.
SQ   SEQUENCE   184 AA;  20753 MW;  982909B6B255DB08 CRC64;


  Query Match             5.2%;  Score 91.5;  DB 1;  Length 184;
  Best Local Similarity   27.4%;  Pred. No. 0.42;
  Matches   26;  Conservative   21;  Mismatches   37;  Indels   11;  Gaps    5;

Qy     135 LRHHHRRWRFTFSHF-VVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVT 193
           : |      |||    |:|| ::|||||:: | :  |:      |||  :  |    :: |
Db      32 IEHKVTEKTFTFKGVNVLDPSKKYEVTLNFLHEVDPE---KVTSKN--IGRC----LEFT 82

Qy     194 TPCMSSGSLWDPNITVETLEAHQLRVSFTLWNEST 228
           |  ::|  |  ::| :  : | |: :|  | : :
Db      83 IPKKAAGPYWS-SLTTDKTKLHFLKANFAKWRDES 116


RESULT   2
VS09_ROTGA
ID   VS09_ROTGA     STANDARD;      PRT;   249 AA.
AC   P18570;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GLYCOPROTEIN VP7 PRECURSOR (OUTER SHELL GLYCOPROTEIN).
GN   S9.
OS   Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
OC   Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX   NCBI_TaxID=12705;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90357782; PubMed=2167559;
RA   Chen G.-M., Hung T., Mackow E.R.;
RT   "Identification of the gene encoding the group B rotavirus VP7
RT   equivalent: primary characterization of the ADRV segment 9 RNA.";
RL   Virology 178:311-315(1990).
CC   -!- FUNCTION: MAJOR OUTER CAPSID PROTEIN.
CC   -!- SIMILARITY: STRONG TO THE VP7 PROTEINS OF THE GROUP A ROTAVIRUSES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M33872; AAA42675.1; -.
DR   PIR; A37080; VGXRHB.
KW   Coat protein; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     15       POTENTIAL.
FT   CHAIN        16    249       GLYCOPROTEIN VP7.
FT   DOMAIN       33     45       CHARGED, HYDROPHILIC REGION.
FT   CARBOHYD     45     45       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     91     91       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   249 AA;  28459 MW;  0BE10CD1C8B2AFB3 CRC64;


  Query Match             5.0%;  Score 88.5;  DB 1;  Length 249;
  Best Local Similarity   22.1%;  Pred. No. 1.1;
  Matches   48;  Conservative   30;  Mismatches   82;  Indels   57;  Gaps    9;

Qy     104 ASILYLEGAELSVLQLN----TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEV 159
           ||:| |  |     |||     |:  :|| :                       |  |
Db       2 ASLLLLVLAAAVTAQLNIVPSTHPEVCVLY--------------------ADDHQ---- 36

Qy     160 TVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMS-SGSLWDPNITVETLEAHQLR 218
                 | |  : ||      |:   :|   || | | :|    :: :  : |
Db      37 ----------ADANKFNGNF--TQIFHSYNSITLSFMSYSSSSYD---VIDIISKYDLS 80

Qy     219 ----VSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLK 274
               ::  ::| |  : : | |  :   ::    :||:  || ||:   |      :|||
Db      81 SCNILAIDVFNASMDFNVFLQSTNNCSKYNA-NKVHHVKLPRGEEWFSYS------KNLK 133

Qy     275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPE 311
           |     |  :  : |:|     :|    |: | ||
Db     134 FCPLSDSLIGMYCDTQLSDTYFEISTGGTYEVTDIPE 170


RESULT   3
SALM_DROVI
ID   SALM_DROVI     STANDARD;      PRT;   1402 AA.
AC   P39806;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   HOMEOTIC PROTEIN SPALT-MAJOR.
GN   SALM.
OS   Drosophila virilis (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7244;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94139659; PubMed=7905822;
RA   Kuehnlein R.P., Frommer G., Friedrich M., Gonzalez-Gaitan M.,
RA   Weber A., Wagner-Bernholz J.F., Gehring W.J., Jaeckle H., Schuh R.;
RT   "Spalt encodes an evolutionarily conserved zinc finger protein of
RT   novel structure which provides homeotic gene function in the head and
RT   tail region of the Drosophila embryo.";
RL   EMBO J. 13:168-179(1994).
CC   -!- FUNCTION: REQUIRED FOR THE ESTABLISHMENT OF THE POSTERIOR-MOST
CC       HEAD AND THE ANTERIOR-MOST TAIL SEGMENTS OF THE EMBRYO. PROBABLY
CC       FUNCTION AS A TRANSCRIPTIONAL REGULATOR. COULD REPRESS THE
CC       TRANSCRIPTION OF THE TSH GENE.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC   -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT BLASTODERM STAGE AND
CC       LATER IN RESTRICTED AERAS OF THE EMBRYONIC NERVOUS SYSTEM AS
CC       WELL AS IN THE DEVELOPING TRACHEA.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z27444; CAA81800.1; -.
DR   PIR; S42748; S42748.
DR   HSSP; P04002; 1WFA.
DR   FlyBase; FBgn0013137; Dvir\salm.
DR   InterPro; IPR000822; -.
DR   Pfam; PF00096; zf-C2H2; 7.
DR   PRINTS; PR00048; ZINCFINGER.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
KW   Developmental protein; Zinc-finger; Metal-binding; DNA-binding;
KW   Nuclear protein; Transcription regulation; Repeat.
FT   ZN_FING      432    454       C2H2-TYPE.
FT   ZN_FING      460    482       C2H2-TYPE.
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FT   ZN_FING      845    867       C2H2-TYPE.
FT   ZN_FING      873    895       C2H2-TYPE.
FT   ZN_FING      905    927       C2H2-TYPE.
FT   ZN_FING     1336   1358       C2H2-TYPE.
FT   ZN_FING     1364   1386       C2H2-TYPE.
SQ   SEQUENCE   1402 AA;  153745 MW;  4CDB2EE384F70AE5 CRC64;

  Query Match             5.0%;  Score 88.5;  DB 1;  Length 1402;
  Best Local Similarity   21.1%;  Pred. No. 9;
  Matches   74;  Conservative   33;  Mismatches  114;  Indels  129;  Gaps   18;

Qy       1 MGAARSPPSAVPGPLLGL------LLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKN 54
           |  | ||  | || | |:      ||  ||  |   | |             |||   :|:
Db     542 MSFASSP--AFPG-LPGIYRPPMELLKSLGATAGSTAGL----PHPFFPQMPGLGAALKH 594

Qy      55 STCLDDSWIHPRNLT----PSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLE 110
           :   | |   | :|     |||| : :  :      : :|      | |::        |
Db     595 TH--DQSQDMPTDLRKSSGPSSPHEEEDNIAARLPVKSELMEEEKTEHTMEAATR----E 648

Qy     111 GAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEY---------EVTV 161
           ||:  | |             ::|     |         :| || :           :|
Db     649 SAEMEPLPL-------------EVRIKEER---------IDEDQMHLQEGMQKPEPLTA 685

Qy     162 HHLPKP----IPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQL 217
           :  | |    ||      :|   |   | |||:          |||
Db     686 YATPHPQQCLIPTTHAAAKSPRSLPLQC-HARL----------SLW-------------- 720

Qy     218 RVSFTLWNESTHYQILLTSFPHMENHSCF------EHMHHIPAP---------RPEEFHQ 262
                         | |   ||:|         |:  :| |         | : | :
Db     721 ----------------CSHPTTSNHACAVLTGSQTHLDQLPTPDNVPPTMPQREDFFAE 763

Qy     263 RSNVTLT--------LRNLKGCCRHQVQIQPFFSSCLNDCLRHSATVSCP 304
           |  :  |        :|:  |     :   |||:     ::|      |
Db     764 RFPLNFTSKTDDHSPIRSPAGHAHAHIPRSPFFNP-----IKHEMAAFVP 808
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RESULT   4
EGFR_HUMAN
ID   EGFR_HUMAN     STANDARD;      PRT;  1210 AA.
AC   P00533; P06268; Q14225;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112).
GN   EGFR OR ERBB1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84219729; PubMed=6328312;
RA   Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
RA   Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
RA   Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
RT   "Human epidermal growth factor receptor cDNA sequence and aberrant
RT   expression of the amplified gene in A431 epidermoid carcinoma cells.";
RL   Nature 309:418-425(1984).
RN   [2]
RP   SEQUENCE OF 713-924 FROM N.A.
RX   MEDLINE=84196372; PubMed=6326261;
RA   Lin C.R., Chen W.S., Kruiger W., Stolarsky L.S., Weber W.,
RA   Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
RT   "Expression cloning of human EGF receptor complementary DNA: gene
RT   amplification and three related messenger RNA products in A431
RT   cells.";
RL   Science 224:843-848(1984).
RN   [3]
RP   SEQUENCE OF 150-962 FROM N.A.
RX   MEDLINE=84245835; PubMed=6330563;
RA   Xu Y., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., Ma D.P.,
RA   Roe B.A., Merlino G.T., Pastan I.;
RT   "Human epidermal growth factor receptor cDNA is homologous to a
RT   variety of RNAs overproduced in A431 carcinoma cells.";
RL   Nature 309:806-810(1984).
RN   [4]
RP   SEQUENCE OF 1028-1210 FROM N.A.
RX   MEDLINE=85046483; PubMed=6093780;
RA   Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
RA   O'Malley B.W.;
RT   "Isolation of an evolutionarily conserved epidermal growth factor
RT   receptor cDNA from human A431 carcinoma cells.";
RL   Biochem. Biophys. Res. Commun. 124:125-132(1984).
RN   [5]
RP   SEQUENCE OF 1-29 FROM N.A.
RX   MEDLINE=88217333; PubMed=3329716;
RA   Haley J., Whittle N., Bennett P., Kinchington D., Ullrich A.,
RA   Waterfield M.;
RT   "The human EGF receptor gene: structure of the 110 kb locus and
RT   identification of sequences regulating its transcription.";
RL   Oncogene Res. 1:375-396(1987).
RN   [6]
RP   SEQUENCE OF 1-29 FROM N.A.
RX   MEDLINE=91107677; PubMed=1988448;
RA   Haley J.D., Waterfield M.D.;
RT   "Contributory effects of de novo transcription and premature
RT   transcript termination in the regulation of human epidermal growth
RT   factor receptor proto-oncogene RNA synthesis.";
RL   J. Biol. Chem. 266:1746-1753(1991).
RN   [7]
RP   SEQUENCE OF 1-29 FROM N.A.
RX   MEDLINE=85270438; PubMed=2991899;
RA   Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;
RT   "Characterization and sequence of the promoter region of the human
RT   epidermal growth factor receptor gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
RN   [8]
RP   SEQUENCE OF 540.
RA   Kohda D.;
RL   Submitted (SEP-1997) to the SWISS-PROT data bank.
RN   [9]
RP   RECEPTOR ACTIVITY.
RX   MEDLINE=84191554; PubMed=6325948;
RA   Mroczkowski B., Mosig G., Cohen S.;
RT   "ATP-stimulated interaction between epidermal growth factor receptor
RT   and supercoiled DNA.";
RL   Nature 309:270-273(1984).
RN   [10]
RP   PHOSPHORYLATION.
RX   MEDLINE=89278137; PubMed=2543678;
RA   Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M.,
RA   Howk R., Givol D., Ullrich A., Schlessinger J.;
RT   "All autophosphorylation sites of epidermal growth factor (EGF)
RT   receptor and HER2/neu are located in their carboxyl-terminal tails.
RT   Identification of a novel site in EGF receptor.";
RL   J. Biol. Chem. 264:10667-10671(1989).
RN   [11]
RP   REVIEW.
RX   MEDLINE=87297456; PubMed=3039909;
RA   Carpenter G.;
RT   "Receptors for epidermal growth factor and other polypeptide
RT   mitogens.";
RL   Annu. Rev. Biochem. 56:881-914(1987).
CC   -!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
CC       AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
CC       VACCINIA VIRUS GROWTH FACTOR.
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC       PROTEIN TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO
CC       INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE
CC       TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS, AND
CC       CELL PROLIFERATION.
CC   -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; X00588; CAA25240.1; -.
DR   EMBL; X06370; CAA29668.1; -.
DR   EMBL; X00663; CAA25282.1; -.
DR   EMBL; M38425; AAA63171.1; -.
DR   EMBL; M11234; AAA52370.1; -.
DR   PIR; A00641; GQHUE.
DR   PIR; A00642; GQHUE2.
DR   PIR; A23062; A23062.
DR   HSSP; P11362; 1FGI.
DR   SWISS-2DPAGE; P00533; HUMAN.
DR   MIM; 131550; -.
DR   InterPro; IPR000494; -.
DR   InterPro; IPR000719; -.
DR   InterPro; IPR001245; -.
DR   InterPro; IPR002174; -.
DR   Pfam; PF00757; Furin-like; 1.
DR   Pfam; PF01030; Recep_L_domain; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transmembrane; Glycoprotein; Duplication; Receptor; Signal;
KW   Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
FT   SIGNAL        1    24
FT   CHAIN        25  1210       EPIDERMAL GROWTH FACTOR RECEPTOR.
FT   DOMAIN       25   645       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    646   668       POTENTIAL.
FT   DOMAIN      669  1210       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       75   300       APPROXIMATE.
FT   REPEAT      390   600       APPROXIMATE.
FT   DOMAIN     1025  1071       SER-RICH.
FT   DOMAIN      712   979       PROTEIN KINASE.
FT   NP_BIND     718   726       ATP (BY SIMILARITY).
FT   BINDING     745   745       ATP (BY SIMILARITY).
FT   ACT_SITE    837   837       BY SIMILARITY.
FT   MOD_RES     678   678       PHOSPHORYLATION (BY PKC).
FT   MOD_RES    1092  1092       PHOSPHORYLATION (AUTO-).
FT   MOD_RES    1110  1110       PHOSPHORYLATION (AUTO-).
FT   MOD_RES    1172  1172       PHOSPHORYLATION (AUTO-).
FT   MOD_RES    1197  1197       PHOSPHORYLATION (AUTO-, MAJOR SITE).
FT   CARBOHYD    128   128       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    175   175       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    196   196       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    352   352       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    361   361       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    413   413       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    444   444       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    528   528       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    568   568       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    603   603       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    623   623       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    540   540       N -> K (IN REF. 1).
SQ   SEQUENCE   1210 AA;  134277 MW;  D8A2A50B4EFB6ED2 CRC64;

  Query Match           5.0%;  Score 88;  DB 1;  Length 1210;
  Best Local Similarity  22.6%;  Pred. No. 8.3;
  Matches   93;  Conservative   45;  Mismatches  156;  Indels  118;  Gaps   22;

Qy      15 LLGLLLL----LLGVLAPGGASLRLL-DHRALVCSQPGLNCTV---KNSTCLDD-SWIH- 64
           |||: |     |:  | | |  |  : :|:  : ||  ||  |   |    |:|   :|
Db     777 LLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRRLVHR 836

Qy      65 ---PRNLTPSSPKDLQIQ-------------------------------LHFAHTQQGD 89
              ||:   :|: ::|                                 ||  :| | |

Db     837 DLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALESILHRIYTHQSD 896

Qy      90 LFPVAHIEWTLQTDASILY--LEGAELSVLQLNTNERL-----CVRFEFL---------S 133
           ::      | | |  |  |  :  :|:| : |   |||     |    ::         :
Db     897 VWSYGVTVWELMTFGSKPYDGIPASEISSI-LEKGERLPQPPICTIDVYMIMVKCWMIDA 955

Qy     134 KLRHHHRRWRFTFSHFVVDPDQEYEVTV----HHLPKPI-----------PDGDPNHQSK 178
             |   |     ||    || | | |         ||| |             | |    :
Db     956 DSRPKFRELIIEFSKMARDP-QRYLVIQGDERMHLPSPTDSNFYRALMDEEDMDDVVDAD 1014

Qy     179 NFLVPDCEHARMKVT--TPCMSSGSLWDPNITVETLEAHQLRV------SF--------- 221
             :|:|         |  || :|| |    | ||  :: : |:       ||
Db    1015 EYLIPQQGFFSSPSTSRTPLLSSLSATSNNSTVACIDRNGLQSCPIKEDSFLQRYSSDPT 1074

Qy     222 -TLWNESTHYQILLT------SFPHMENHSCFEHMHH----IPAPRPEEFHQRSNVTLTL 270
              |  :|    |         | |     |    ::|     |||  :  :|  : |
Db    1075 GALTEDSIDDTFLPVPEYINQSVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAV- 1133

Qy     271 RNLKGCCRHQVQIQPFFSSCLN---DCLRHSATVSCPEMP-DTPEPIPDYMP 318
             |    :   :||   :|:|   |   | |     ::  | |:   |: |
Db    1134 ----GNPEYLNTVQP---TCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFP 1178


RESULT   5
SYEP_DROME
ID   SYEP_DROME     STANDARD;       PRT;  1714 AA.
AC   P28668; Q9VCF5;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   BIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA
DE   SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA
DE   SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)].
GN   AATS-GLUPRO OR CG5394.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92097547; PubMed=1756734;
RA   Cerini C., Kerjan P., Astier M., Gratecos D., Mirande M., Semeriva M.;
RT   "A component of the multisynthetase complex is a multifunctional
RT   aminoacyl-tRNA synthetase.";
RL   EMBO J. 10:4267-4277(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OREGON-R;
RX   MEDLINE=97217441; PubMed=9063462;
RA   Cerini C., Semeriva M., Gratecos D.;
RT   "Evolution of the aminoacyl-tRNA synthetase family and the
RT   organization of the Drosophila glutamyl-prolyl-tRNA synthetase gene.
RT   Intron/exon structure of the gene, control of expression of the two
RT   mRNAs, selective advantage of the multienzyme complex.";
RL   Eur. J. Biochem. 244:176-185(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA   Dodson K., Doup L.E., Downes M., Duqan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC       PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC   -!- CATALYTIC ACTIVITY: ATP + L-PROLINE + TRNA(PRO) = AMP +
CC       PYROPHOSPHATE + L-PROLYL-TRNA(PRO).
CC   -!- SUBUNIT: COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH IS
CC       COMPRISED OF A BIFUNCTIONAL GLUTAMYL-PROLYL-TRNA SYNTHETASE, THE
CC       MONOSPECIFIC ISOLEUCYL, LEUCYL, GLUTAMINYL, METHIONYL, LYSYL,
CC       ARGINYL, AND ASPARTYL-TRNA SYNTHETASES AS WELL AS THREE AUXILIARY
CC       PROTEINS, P18, P48 AND P43.
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CLASS-I
CC       AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-II
CC       AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   -!- SIMILARITY: CONTAINS 6 "WHEP-TRS" DOMAINS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M74104; AAA28594.1; -.
DR   EMBL; U59923; AAC47469.1; -.
DR   EMBL; AE003745; AAF56211.1; -.
DR   PIR; S18644; S18644.
DR   HSSP; P00962; 1QRU.
DR   FlyBase; FBgn0005674; Aats-glupro.
DR   InterPro; IPR000738; -.
DR   InterPro; IPR000924; -.
DR   InterPro; IPR001412; -.
DR   InterPro; IPR002106; -.
DR   InterPro; IPR002314; -.
DR   InterPro; IPR002316; -.
DR   Pfam; PF00458; WHEP-TRS; 6.
DR   Pfam; PF00749; tRNA-synt_1c; 1.
DR   Pfam; PF00587; tRNA-synt_2b; 1.
DR   PRINTS; PR00987; TRNASYNTHGLU.
DR   PRINTS; PR01046; TRNASYNTHPRO.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR   PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
DR   PROSITE; PS00762; WHEP_TRS; 6.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Multifunctional enzyme; Repeat.
FT   DOMAIN      170     754       GLUTAMYL-TRNA SYNTHETASE.
FT   DOMAIN      755     800       WHEP-TRS 1.
FT   DOMAIN      827     872       WHEP-TRS 2.
FT   DOMAIN      901     946       WHEP-TRS 3.
FT   DOMAIN      980     1025      WHEP-TRS 4.
FT   DOMAIN      1055    1100      WHEP-TRS 5.
FT   DOMAIN      1129    1173      WHEP-TRS 6.
FT   DOMAIN      1174    1180      POLY-GLY.
FT   DOMAIN      1207    1714      PROLYL-TRNA SYNTHETASE.
FT   SITE        209     220       "HIGH" REGION.
FT   SITE        438     442       "KMSKS" REGION.
FT   BINDING     441     441       ATP (BY SIMILARITY).
FT   CONFLICT    102     106       TSPLP -> DKSIA (IN REF. 3).
FT   CONFLICT    233     234       VC -> AF (IN REF. 3).
FT   CONFLICT    341     345       NTACA -> KYCVR (IN REF. 3).
FT   CONFLICT    583     583       K -> R (IN REF. 3).
FT   CONFLICT    692     692       L -> A (IN REF. 3).
FT   CONFLICT    753     753       T -> S (IN REF. 3).
FT   CONFLICT    802     802       T -> S (IN REF. 3).
FT   CONFLICT    873     873       P -> T (IN REF. 3).
FT   CONFLICT    887     887       G -> V (IN REF. 3).
FT   CONFLICT    1201    1201      P -> PA (IN REF. 3).
FT   CONFLICT    1461    1461      MISSING (IN REF. 3).
FT   CONFLICT    1587    1587      G -> V (IN REF. 3).
SQ   SEQUENCE   1714 AA;  189197 MW;  6FE8C58045E48A8C CRC64;

  Query Match           5.0%;  Score 87.5;  DB 1;  Length 1714;
  Best Local Similarity  19.2%;  Pred. No. 14;
  Matches   71;  Conservative   48;  Mismatches  119;  Indels  131;  Gaps   17;

Qy      32 SLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSP----------KDLQIQ-- 79
           ||:  |:| |||             |:  |       | |  ::|           :  ||
Db      39 SLQFPDNRLLVCH--------SNNDVL-------RALARAAPDYKLYGETAIERTQIDHW 83

Qy      80 LHFAHTQQGDLFPVAHIEWTLQTDAS----ILYLEGAELSVLQLNTNERLCVRFEFLSK- 134
           | |: | : |      | | |     |    : ||   :|::         :  |:|||:
Db      84 LSFSLTCEDD------ISWALSFLTSPLPPVTYLVANKLTIADFALFNEMHSRYEFLAAK 137

Qy     135 -LRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPK--------------PIPDGDPNHQSK 178
            :  | :||     : ::        :  :  ||:                |  |:   : |
Db     138 GIPQHVQRW-----YDLITAQPLIQKVLQSLPEDAKVKRSPQSSKEQTPAKTGERKQEGK 192

Qy     179 NFLVPDCEHARMKVTTPCMSSGSLW-------------------------DPNITVETL 212
           :|  |  :: |  |  :|| |                           |  |   ||:
Db     193 FVDLPGAEMGKVVVRFPPEASGYLHIGHAKAALLNQYYALVCQGTLIMRFDDTNPAKETV 252

Qy     213 E--------AHQLRVSFTLWNESTHYQILLTSFPHMENHSCF----EHMHHIPAPRPE-- 258
           |          ||::   ::  :::|  |:  :       |      |   ::    ||
Db     253 EFENVILGDLEQLQIKPDVFTHTSNYFDLMLDY-------CVRLIKESKAYVDDTPPEQM 305

Qy     259 --EFHQR-----------SNVTLTLRNLKG-------CCRHQVQIQPFFSSCLNDCLRHS 298
             |  ||           |::|    :||          |  :: :     |  | |:|
Db     306 KLEREQRVESANRSNSVEKNLSLWEEMVKGSEKGQNTACAAKIDM-----SSPNGCMRDP 360

Qy     299 ATVSCPEMP 307
           |   |
Db     361 TIYRCKNEP 369


RESULT   6
XYLA_HAEIN
ID   XYLA_HAEIN     STANDARD;      PRT;   439 AA.
AC   P44398;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   XYLOSE ISOMERASE (EC 5.3.1.5).
GN   XYLA OR HI1112.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
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```
RC   STRAIN=RD / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus
RT   influenzae Rd.";
RL   Science 269:496-512(1995).
CC   -!- CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.
CC   -!- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY (BY SIMILARITY).
CC   -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; U32791; AAC22766.1; -.
DR   HSSP; P45687; 1A0E.
DR   TIGR; HI1112; -.
DR   InterPro; IPR001998; -.
DR   Pfam; PF00259; Xylose_isom; 1.
DR   PRINTS; PR00688; XYLOSISMRASE.
DR   PROSITE; PS00172; XYLOSE_ISOMERASE_1; 1.
DR   PROSITE; PS00173; XYLOSE_ISOMERASE_2; 1.
KW   Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
FT   ACT_SITE    101    101       BY SIMILARITY.
FT   METAL       232    232       MAGNESIUM (BY SIMILARITY).
FT   METAL       268    268       MAGNESIUM (BY SIMILARITY).
FT   METAL       296    296       MAGNESIUM (BY SIMILARITY).
FT   METAL       339    339       MAGNESIUM (BY SIMILARITY).
SQ   SEQUENCE   439 AA;  49896 MW;  24CD3CE4736A3EA6 CRC64;

  Query Match             4.9%;  Score 86;  DB 1;  Length 439;
  Best Local Similarity  20.6%;  Pred. No. 3.6;
  Matches   47;  Conservative   34;  Mismatches   71;  Indels   76;  Gaps   10;

Qy      76 LQIQLHFAHT---QQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLNTNERLCVRFEFL 132
           |:: : : ||      |:| :  :| : | ::::  | |||         ::  : ||||
Db      42 LRLAVCYWHTFCWNGNDMFGLGSLERSWQKNSNL--LAGAE---------QKADIAFEFL 90

Qy     133 SKLRHHHRRWRFTFSHFVVDPD----QEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHA 188
           :|| :   : |   : |:   :|| ||                :|  |
Db      91 NKLGVPY----YCFHDVDIAPEGNSVREYVQNFHH----------------IVDILERK 129

Qy     189 RMKV-----------TTPCMSSGSLWDPNITVETLEAHQL----------RVSFTLWN 225
           ::: :           | |   ||:  :|| |   | |:            :: ||
Db     130 QVETGVKLLWGTANCFTNPRYMSGAATNPNPEVFAWAATQVFNAMNATQRLGGENYVLWG 189

Qy     226 ESTHYQILLTSFPHMENHS-------CFEHMHHIP-------APRPEE 259
           |: || :    |              || | |          |:|:|
Db     190 GREGYETLLNTDLKRKREQIGRFMQMVVEHKHKIGFKGTLLIEPKPQE 237


RESULT   7
DOPO_HUMAN
ID   DOPO_HUMAN      STANDARD;      PRT;   603 AA.
AC   P09172;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-
DE   HYDROXYLASE) (DBH).
GN   DBH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89160241; PubMed=2922261;
RA   Kobayashi K., Kurosawa Y., Fukita K., Nagatsu T.;
RT   "Human dopamine beta-hydroxylase gene: two mRNA types having
RT   different 3'-terminal regions are produced through alternative
RT   polyadenylation.";
RL   Nucleic Acids Res. 17:1089-1102(1989).
RN   [2]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=88166633; PubMed=3443096;
RA   Lamouroux A., Vigny A., Faucon Biguet N., Darmon M.C., Franck R.,
RA   Henry J.-P., Mallet J.;
RT   "The primary structure of human dopamine-beta-hydroxylase: insights
RT   into the relationship between the soluble and the membrane-bound
RT   forms of the enzyme.";
RL   EMBO J. 6:3931-3937(1987).
CC   -!- FUNCTION: CONVERSION OF DOPAMINE TO NORADRENALINE.
CC   -!- CATALYTIC ACTIVITY: 3,4-DIHYDROXYPHENETHYLAMINE + ASCORBATE + O(2)
CC       = NORADRENALINE + DEHYDROASCORBATE + H(2)O.
CC   -!- COFACTOR: PQQ, COPPER, AND ASCORBATE.
CC   -!- PATHWAY: CATECHOLAMINE BIOSYNTHESIS.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SUBCELLULAR LOCATION: EXISTS BOTH IN A SOLUBLE FORM (IN CHROMAFFIN
CC       GRANULES) AND AS MEMBRANE BOUND (THE MEMBRANE BOUND FORM IS
CC       ANCHORED BY AN UNCLEAVED SIGNAL PEPTIDE).
CC   -!- INDUCTION: ACTIVITY IS ENHANCED BY NERVE GROWTH FACTOR (IN
CC       SUPERIOR CERVICAL GANGLIA & ADRENAL MEDULLA). TRANS-SYNAPTIC
CC       STIMULATION WITH RESERPINE, ACETYLCHOLINE AND GLUCOCORTICOIDS.
CC   -!- POLYMORPHISM: THERE EXIST TWO FORMS OF DBH: DBH-A AND DBH-B,
CC       WHICH DIFFER IN ONE POSITION.
CC   -!- SIMILARITY: BELONGS TO THE COPPER TYPE II, ASCORBATE-DEPENDENT
CC       MONOOXYGENASE FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; X13255; CAA31631.1; -.
DR   EMBL; X13256; CAA31632.1; -.
DR   EMBL; Y00096; CAA68285.1; -.
DR   PIR; S03020; S03020.
DR   PIR; S06283; S06283.
DR   MIM; 223360; -.
DR   InterPro; IPR000323; -.
DR   InterPro; IPR000945; -.
DR   Pfam; PF01082; Cu2_monooxygen; 1.
DR   PRINTS; PR00767; DBMONOXGNASE.
DR   PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
DR   PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.
KW   Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Copper;
KW   Vitamin C; PQQ; Glycoprotein; Membrane; Signal; Polymorphism.
FT   SIGNAL        1     25
FT   CHAIN        26    603       DOPAMINE BETA-MONOOXYGENASE.
FT   ACT_SITE    216    216       POTENTIAL.
FT   ACT_SITE    398    398       POTENTIAL.
FT   BINDING     398    398       COPPER (POTENTIAL).
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    330    330       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    552    552       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     304    304       A -> S (IN DBH-B).
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FT                              /FTId=VAR_002196.
FT   CONFLICT    197    197     A -> T (IN REF. 2).
FT   CONFLICT    535    535     R -> C (IN REF. 2).
SQ   SEQUENCE   603 AA;  67627 MW;  39A7A8975111DB5F CRC64;

  Query Match             4.9%;  Score 86;  DB 1;  Length 603;
  Best Local Similarity   19.4%;  Pred. No. 5.3;
  Matches   54;  Conservative   42;  Mismatches  110;  Indels   72;  Gaps   14;

Qy      68 LTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL-------------QTDASILY----- 108
           |  |:|::  :  |     :| |     : | :             :  | :|:
Db      23 LQGSAPRESPLPYHIPLDPEGSL----ELSWNVSYTQEAIHFQLLVRRLKAGVLFGMSDR 78

Qy     109 --LEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYE-VTVHHLP 165
           || |:| ||  :           :     |          :|| |:|: : |   |
Db      79 GELENADLVVLWTD-----------GDTAYFADAWSDQKGQIHLDPQQDYQLLQVQRTP 126

Qy     166 --------KPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQL 217
                  :|    ||    |::|: |         |  :  | | :|  ::| :    |
Db     127 EGLTLLFKRPFGTCDP----KDYLIED--------GTVHLVYGILEEPFRSLEAINGSGL 174

Qy     218 RVSFTLWNESTHYQILLTSFPHME--NHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNL-K 274
           ::          |:|  : |  |  : :|     : ||  :   | :    :: | |
Db     175 QMGL------QRVQLLKPNIPEPELPSDAC---TMEVQAPNIQIPSQETTYWCYIKELPK 225

Qy     275 GCCRHQ-VQIQPFFSSCLNDCLRHSATVSC-PEMPDTP 310
           |  ||  :: :|  :     : |     | |||   |
Db     226 GFSRHHIIKYEPIVTKGNEALVHHMEVFQCAPEMDSVP 263


RESULT   8
KAIB_SCHPO
ID   KAIB_SCHPO     STANDARD;      PRT;   607 AA.
AC   Q09898;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   PROBABLE SERINE/THREONINE-PROTEIN KINASE C24B11.11C (EC 2.7.1.-).
GN   SPAC24B11.11C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Odell C., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC       PROTEIN KINASES. HIGHLY SIMILAR TO YEAST DBF20 AND DBF2.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z67757; CAA91776.1; -.
DR   HSSP; P05132; 1CTP.
DR   InterPro; IPR000719; -.
DR   InterPro; IPR000961; -.
DR   InterPro; IPR002290; -.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW   ATP-binding; Phosphorylation.

FT   DOMAIN      208    508     PROTEIN KINASE.
FT   NP_BIND     214    222     ATP (BY SIMILARITY).
FT   BINDING     237    237     ATP (BY SIMILARITY).
FT   ACT_SITE    331    331     BY SIMILARITY.
FT   MOD_RES     219    219     PHOSPHORYLATION (BY SIMILARITY).
SQ   SEQUENCE   607 AA;  70491 MW;  D92E5263C7341F1D CRC64;

  Query Match             4.8%;  Score 85;  DB 1;  Length 607;
  Best Local Similarity   21.7%;  Pred. No. 6.5;
  Matches   60;  Conservative   30;  Mismatches   85;  Indels  102;  Gaps   14;

Qy      89 DLFPVAHIEWTLQ-----TDASILYL-----EGAELSVLQLNTNERLCVRFEFLSKLRHH 138
           |:   |: || ::      | | :||      | :   |  |:           || |
Db     258 DILTTANSEWLVRLLYAFQDTSNIYLAMEFVPGGDFRTLLSNS----------GVLRDH 306

Qy     139 HRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMS 198
           | ::  |     :|        :| |     |  |    :|||    |  :|:|   :|
Db     307 HAKFYATEMFLAID-------ALHQLGYIHRDLKP----ENFLVGASGH--IKLTDFGLS 353

Qy     199 SGSLWDP------------NITVETLEAHQLRVSF-TL-------------------- 223
           || :                |: |     : |  | ||
Db     354 SGIISKKKIESMKIRLQEVNNVVVPERSMRERRQVFRTLLSQDPVYAHSVVGSPDYMAPE 413

Qy     224 ------WNESTHYQIL-------LTSFP------------HMEN-HSCFEHMHHIPAPRP 257
                :| |  | |         |: ||             :::|   ||:  |:   ||
Db     414 VLRGENYNHSVDYWSLGCIMYECLSGFPPFSGSNVNETWSNLKNWRKCFQRPHY-DDPRD 472

Qy     258 EEFHQRSNV------TLTLRNLKGCCRHQVQIQPFFS 288
           ||: | :         :|    : |   ||   |:||
Db     473 LEFNWRDDAWDFVCHCITDPKDRFCSLKQVMQHPYFS 509


RESULT   9
GEM4_HUMAN
ID   GEM4_HUMAN     STANDARD;      PRT;  1058 AA.
AC   P57678;
DT   01-OCT-2000 (Rel. 40, Created)
DT   01-OCT-2000 (Rel. 40, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   COMPONENT OF GEMS 4 (GEMIN4) (P97).
GN   GEMIN4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MASS SPECTROMETRY.
RX   MEDLINE=20191885; PubMed=10725331;
RA   Charroux B., Pellizzoni L., Perkinson R.A., Yong J., Shevchenko A.,
RA   Mann M., Dreyfuss G.;
RT   "Gemin4: a novel component of the SMN complex that is found in both
RT   gems and nucleoli.";
RL   J. Cell Biol. 148:1177-1186(2000).
CC   -!- FUNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOSOMAL
CC       SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA
CC       SPLICING IN THE NUCLEUS. GEMIN4 COULD SERVE AS A COFACTOR OF
CC       GEMIN3.
CC   -!- SUBUNIT: FORMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR
CC       NEURON PROTEIN (SMN), GEMIN2 AND GEMIN3. INTERACTS DIRECTLY WITH
CC       GEMIN3 AND WITH SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B',
CC       D1-D3, AND E.
CC   -!- SUBCELLULAR LOCATION: CYTOPLAMIC AND NUCLEAR. LOCALIZED IN
CC       SUBNUCLEAR STRUCTURES NEXT TO COILED BODIES, CALLED GEMS, WHICH
CC       ARE HIGHLY ENRICHED IN SPLICEOSOMAL SNRNPS AND IN THE NUCLEOLUS.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF173856; AAF35283.1; -.
KW   mRNA processing; Spliceosome; Nuclear protein.
FT   DOMAIN       714    735       LEUCINE-ZIPPER (POTENTIAL).
SQ   SEQUENCE   1058 AA;  119989 MW;  5EE1FE2EE3538D6B CRC64;


  Query Match              4.8%;  Score 84.5;  DB 1;  Length 1058;
  Best Local Similarity   19.5%;  Pred. No. 14;
  Matches   66;  Conservative   36;  Mismatches  115;  Indels  121;  Gaps   16;

Qy      63 IHPRNLTPSSPKD-LQIQLHFAHTQQGDLFPVAH----IEWTLQTDASILYLEGAELSVL 117
           : |  :|||  :   |  | |:    |:: |  :      |     :|| |:::     |
Db      78 LQPHPVTPSDTETRWQEDLFFS---VGNMIPTINHTILFELLKSLEASGLFIQ------L 128

Qy     118 QLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQE---------YEVTVH------ 162
           :     :|          |    ||   |  ||   |           :|| |
Db     129 LMALPTTIC----------HAELERF-LEHVTVDTSAEDVAFFLDIWWEVMKHKGHPQD 176

Qy     163 --------------------HLPKPI---PDGDPNHQSKNFLVPDCEHARMKVTTP--- 195
                               | || :   ||  |      |:      : ::  |
Db     177 PLLSQFSAMAHKYLPALDEFPHPPKRLRSDPDACPTMPLLAMLLRGLTQIQSRILGPGRK 236

Qy     196 CMSSGSLW----------DPNITVETLEAHQLRVSFTLWNEST----HYQIL------- 233
           | :  :|            ||     |:   :|    ::||  |     | |
Db     237 CCALANLADMLTVFALTEDDPQEVSATVYLDKLATVISVWNSDTQNPYHQQALAEKVKEA 296

Qy     234 -----LTSFPHMENHSCF---EHMHHIPAPRPEEFHQ---------------------R 263
                |||   : : : |   | :||:     ||
Db     297 ERDVSLTSLAKLPSETIFVGCEFLHHLLREWGEELQAVLRSSQGTSYDSYRLCDSLTSFS 356

Qy     264 SNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSATV 301
           | || | |      :   |:     : |: | || ::||
Db     357 QNATLYL-NRTSLSKEDRQVVSELAECVRDFLRKTSTV 393


RESULT  10
INF_ANAPL
ID   INF_ANAPL      STANDARD;      PRT;   191 AA.
AC   P51526;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   INTERFERON PRECURSOR.
GN   IFN.
OS   Anas platyrhynchos (Domestic duck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX   NCBI_TaxID=8839;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=96010237; PubMed=7571434;
RA   Schultz U., Koeck J., Schlicht H.J., Staeheli P.;
RT   "Recombinant duck interferon: a new reagent for studying the mode of
RT   interferon action against hepatitis B virus.";
RL   Virology 212:641-649(1995).
CC   -!- INDUCTION: BY VIRUSES.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X84764; CAA59235.1; -.
DR   HSSP; P01574; 1AU1.
DR   InterPro; IPR000471; -.
DR   Pfam; PF00143; interferon; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Glycoprotein; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    191       INTERFERON.
FT   DISULFID    31    128       BY SIMILARITY.
FT   DISULFID    67    167       BY SIMILARITY.
FT   DISULFID    60    154       POTENTIAL.
FT   CARBOHYD    77     77       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   191 AA;  21651 MW;  54D197AC899BB82F CRC64;


  Query Match              4.7%;  Score 83;  DB 1;  Length 191;
  Best Local Similarity   20.5%;  Pred. No. 2.4;
  Matches   56;  Conservative   29;  Mismatches   70;  Indels  118;  Gaps   15;

Qy       8 PSAVPGP-LLGLLLLLLGVLAPGGA----------------SLRLLDHRALVCSQPGLNC 50
           ||| | | :   | |||  :  | |                  ||:|| : |   :||   |
Db       4 PSAPPPPAIYSALALLLLLTPPANAFSCSPLRLHDSAFAWDSLQLLRNMAPSPTQP---C 60

Qy      51 TVKNSTC-LDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYL 109
             ::: |   |: :   :   ::   | : |     |       | ||  |
Db      61 PQQHAPCSFPDTLLDTNDTQQAAHTALHLLQHLFDTLSSPSTP-AH--W---------- 106

Qy     110 EGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIP 169
               |:|      | : |::|:||                                :||| :  |
Db     107 ---------LHT-----ARHDLLNQLQHH---------------------IHHLERCFP 130

Qy     170 --------DGDPN-HQSKNFLVPDCEHARMKVT-TPCMSSGSLWDPNITVETLEAHQLRV 219
                   |  | | | |          :|     | :||      ||
Db     131 ADAARLHRRGPRNLHLSINKYFGCIQHFLQNHTYSPC-----AWD---------------- 170

Qy     220 SFTLWNESTHYQILLTSFPHMENHSCFEHMHHI 252
               | :          :| |:||: :| :
Db     171 ---------HVR--------LEAHACFQRIHRL 186


RESULT  11
RPB3_MOUSE
ID   RPB3_MOUSE     STANDARD;      PRT;   275 AA.
AC   P97760;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   DNA-DIRECTED RNA POLYMERASE II 33 KDA POLYPEPTIDE (EC 2.7.7.6) (RPB3)
DE   (RNA POLYMERASE II SUBUNIT 3) (RPB33) (RPB31).
GN   POLR2C OR RPO2-3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97186689; PubMed=9034305;
RA   Korobko I.V., Yamamoto K., Nogi Y., Muramatsu M.;
RT   "Protein interaction cloning in yeast of the mouse third largest RNA
RT   polymerase II subunit, mRPB31.";
RL   Gene 185:1-4(1997).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC       RNA(N).
CC   -!- SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC       FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC       PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC       III FOR 5S AND TRNA GENES.
CC   -!- SIMILARITY: BELONGS TO THE RPB3/RPC5 RNA POLYMERASE SUBUNIT
CC       FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; D83999; BAA12205.1; -.
DR   MGD; MGI:109299; Rpo2-3.
DR   InterPro; IPR001514; -.
DR   PROSITE; PS00446; RNA_POL_D_30KD; 1.
DR   Transferase; DNA-directed RNA polymerase; Transcription;
KW   Nuclear protein.
KW   DOMAIN      88     97     CYS-RICH.
FT   SEQUENCE   275 AA;  31311 MW;  8D6831CCBAD5D82C CRC64;
SQ

Query Match             4.7%;  Score 83;  DB 1;  Length 275;
Best Local Similarity  20.3%;  Pred. No. 3.7;
Matches   44;  Conservative   30;  Mismatches   79;  Indels   64;  Gaps    8;

Qy      54 NSTCLDDSWI-HPRNLTPSSPKDLQIQLHFAHTQQGDLF-PVAHIEWTLQ--------- 101
           ||: | | :| | | | :  :| ::      : | |   :|:||
Db      55 NSSVLHDEFIAHRLGLIPLTSDDIVDKLQYSRDCTCEEFCPECSVEFTLDVRCNEDQTRH 114

Qy     102 -TDASIL----------------YLEGAELSVLQLNTNERLCVRFEFLSKLRHHHR 140
           |  ::                |:|  :: :::|   : | :|    :    |
Db     115 VTSRDLISNSPRVIPVTSRNRDNDPNDYVEQDDILIVKLRKGQELRLRAYVKKRSGKEHA 174

Qy     141 RWRFTFS-HFVVDPDQEYEVTVHHLPKPIPDG----------DPNHQSKNFL--VP 183
           :| |   |  |||     ||:  |: |           |||  : : |      |
Db     175 KWNPTAGVAFEYDPDNGLRHTVYPKPEEGPKSEYSELDEDESQAPYDPNGKPERFYYNVE 234

Qy     184 DCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVS 220
           |           |||     |  :   |   : ::|
Db     235 SC----------GSLRPETIGLSALSGLKKKLS 257


RESULT  12
PURL_LACCA      STANDARD;       PRT;   740 AA.
ID   PURL_LACCA
AC   P35852;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM
DE   SYNTHASE II).
GN   PURL.
OS   Lactobacillus casei.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC   Lactobacillus.
OX   NCBI_TaxID=1582;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93012962; PubMed=1398079;
RA   Gu Z.-M., Martindale D.W., Lee B.H.;
RT   "Isolation and complete sequence of the purL gene encoding FGAM
RT   synthase II in Lactobacillus casei.";
RL   Gene 119:123-126(1992).
RN   [2]
RP   REVISIONS.
RX   MEDLINE=94040790; PubMed=8224889;
RA   Gu Z.-M., Martindale D.W., Lee B.H.;
RL   Gene 133:147-147(1993).
CC   -!- CATALYTIC ACTIVITY: ATP + 5'-PHOSPHORIBOSYLFORMYLGLYCINAMIDE +
CC       L-GLUTAMINE + H(2)O = ADP + ORTHOPHOSPHATE + 5'-PHOSPHORIBOSYL-
CC       FORMYLGLYCINAMIDINE + L-GLUTAMATE.
CC   -!- PATHWAY: FOURTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
CC   -!- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.
CC   -!- SIMILARITY: BELONGS TO THE FGAMS FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M85265; AAC36947.1; -.
DR   PIR; JC1290; JC1290.
DR   InterPro; IPR000728; -.
DR   Pfam; PF00586; AIRS; 2.
DR   Purine biosynthesis; Ligase; ATP-binding.
KW   NP_BIND     112    123
FT   SEQUENCE   740 AA;  79481 MW;  03238AB3CD1C8FF5 CRC64;
SQ

Query Match             4.7%;  Score 83;  DB 1;  Length 740;
Best Local Similarity  21.3%;  Pred. No. 12;
Matches   74;  Conservative   36;  Mismatches  102;  Indels  136;  Gaps   20;

Qy      25 VLAPG--GASLRLL-DHRALVCS--QPGLNCTVKNSTCLDDSWI-HPRNLTPSSPKDLQI 78
           |: ||   | :|:  ||||  :      : | :    | :: |:   |||   | : | |
Db     440 VVLPGSDAAVIRIRGTHRALAMTTDSKDVTCILIAGGCGNECWLKRARNLVASGAEPLGI 499

Qy      79 Q--LHFAHTQQGDLF----------------PV--AHIEWTLQTDASILY------- 108
           |:|     : : |                  ||   ::    :|:   :|
Db     500 TDCLNFGDPTKPEAFYELAEAAKGIIAATKAFNAPVISGNVSLYNETNGEAIYPTPMIGM 559

Qy     109 ----------------------------LEGAELSVLQLNTNERLCVRFEFLSKLRH 137
                                        |:|| ||  | |    |:|  :
Db     560 VGLIEDLSTITTAAFKQADDLIYLVGETHGDFNGSELQKLQ--TGEVTGKLFDFDLEAEK 617

Qy     138 HHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCE------HARM 190
           |:  |||:  :|: :|    .: ||          ||    |          |::
Db     618 QHQ------HFVLKAIREHLITAAH---DLSDG------GLLVALAEMGFDAQLGAQI 660

Qy     191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNES-THYQILLTSFPHMENHSCFEHM 249
           || |                          | | | |  : ||| |  || : || :
Db     661 NVTLP----------PRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCL 291

Qy     250 HHIPA------PRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCL 291
           |  ||       | ||     ||   ::     :  |:|  |  |
Db     693 HG-PAQLIGRVQAPPEF----EVTTVNQHFSASLQ---QLQTAFEEAL 732


RESULT  13
LMP1_HUMAN      STANDARD;       PRT;   416 AA.
ID   LMP1_HUMAN
AC   P11279;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 1 PRECURSOR (LAMP-1)
DE   (CD107A ANTIGEN).
GN   LAMP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 28-50; 116-130 AND 163-197.
RX   MEDLINE=89066687; PubMed=3198605;
RA   Fukuda M., Viitala J., Matteson J., Carlsson S.R.;
RT   "Cloning of cDNAs encoding human lysosomal membrane glycoproteins, h-
RT   lamp-1 and h-lamp-2. Comparison of their deduced amino acid
RT   sequences.";
RL   J. Biol. Chem. 263:18920-18928(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=93232065; PubMed=8517882;
RA   Sawada R., Jardine K.A., Fukuda M.;
RT   "The genes of major lysosomal membrane glycoproteins, lamp-1 and
RT   lamp-2. 5'-flanking sequence of lamp-2 gene and comparison of exon
```

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RT   organization in two genes.";
RL   J. Biol. Chem. 268:9014-9022(1993).
RN   [3]
RP   SEQUENCE OF 32-416 FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=88234502; PubMed=3131762;
RA   Viitala J., Carlsson S.R., Siebert P.D., Fukuda M.;
RT   "Molecular cloning of cDNAs encoding lamp A, a human lysosomal
RT   membrane glycoprotein with apparent Mr approximately equal to
RL   120,000.";
RN   [4]
RP   SEQUENCE OF 28-58.
RX   MEDLINE=89104438; PubMed=2912382;
RA   Mane S.M., Marzella L., Bainton D.F., Holt V.K., Cha Y.,
RA   Hildreth J.E.K., August J.T.;
RT   "Purification and characterization of human lysosomal membrane
RT   glycoproteins.";
RL   Arch. Biochem. Biophys. 268:360-378(1989).
RN   [5]
RP   DISULFIDE BONDS.
RX   MEDLINE=90062189; PubMed=2584229;
RA   Carlsson S.R., Fukuda M.;
RT   "Structure of human lysosomal membrane glycoprotein 1. Assignment of
RT   disulfide bonds and visualization of its domain arrangement.";
RL   J. Biol. Chem. 264:20526-20531(1989).
RN   [6]
RP   POLYLACTOSAMINOGLYCANS.
RX   MEDLINE=91056099; PubMed=2243102;
RA   Carlsson S.R., Fukuda M.;
RT   "The polylactosaminoglycans of human lysosomal membrane glycoproteins
RT   lamp-1 and lamp-2. Localization on the peptide backbones.";
RL   J. Biol. Chem. 265:20488-20495(1990).
RN   [7]
RP   CARBOHYDRATE-LINKAGE SITES IN HINGE REGION, AND SEQUENCE OF 190-214.
RX   MEDLINE=93312023; PubMed=8323299;
RA   Carlsson S.R., Lycksell P.-O., Fukuda M.;
RT   "Assignment of O-glycan attachment sites to the hinge-like regions of
RT   human lysosomal membrane glycoproteins lamp-1 and lamp-2.";
RL   Arch. Biochem. Biophys. 304:65-73(1993).
CC   -!- FUNCTION: PRESENTS CARBOHYDRATE LIGANDS TO SELECTINS. ALSO
CC       IMPLICATED IN TUMOR CELL METASTASIS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. LYSOSOMAL.
CC       THIS PROTEIN SHUTTLES BETWEEN LYSOSOMES, ENDOSOMES, AND THE PLASMA
CC       MEMBRANE.
CC   -!- PTM: O- AND N-GLYCOSYLATED; SOME OF THE 18 N-GLYCANS ATTACHED TO
CC       LAMP-1 ARE POLYLACTOSAMINOGLYCANS.
CC   -!- SIMILARITY: BELONGS TO THE LAMP FAMILY.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD107a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd107a.htm".
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; J04182; AAA60382.1; -.
DR   EMBL; J03263; AAA59524.1; -.
DR   PIR; A23656; A23656.
DR   PIR; A30210; A30210.
DR   PIR; A31959; A31959.
DR   PIR; A32685; A32685.
DR   PIR; S02150; S02150.
DR   PIR; B46044; B46044.
DR   GlycoSuiteDB; P11279; -.
DR   CarbBank; CCSD:5474; -.
DR   CarbBank; CCSD:5478; -.
DR   MIM; 153330; -.
DR   InterPro; IPR002000; -.
DR   Pfam; PF01299; Lamp; 1.
DR   PRINTS; PR00336; LYSASSOCTDMP.
DR   PROSITE; PS00310; LAMP_1; 2.
DR   PROSITE; PS00311; LAMP_2; 1.
KW   Transmembrane; Glycoprotein; Lysosome; Signal.
FT   SIGNAL       1     27
FT   CHAIN       28    416       LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN
FT                                1.
FT   DOMAIN       28    381       LUMENAL (POTENTIAL).
FT   TRANSMEM    382    404       POTENTIAL.
FT   DOMAIN      405    416       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       28    193       FIRST LUMENAL DOMAIN.
FT   DOMAIN      194    226       HINGE.
FT   DISULFID    227    381       SECOND LUMENAL DOMAIN.
FT   DISULFID     40     79
FT   DISULFID    154    190
FT   DISULFID    230    268
FT   CARBOHYD    337    374
FT   CARBOHYD     36     36
FT   CARBOHYD     44     44       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     61     61       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     75     75       POLYLACTOSAMINOGLYCAN.
FT   CARBOHYD     83     83       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    120    120       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    129    129       POLYLACTOSAMINOGLYCAN.
FT   CARBOHYD    164    164       POLYLACTOSAMINOGLYCAN.
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    196    196       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    198    198       PARTIAL.
FT   CARBOHYD    199    199
FT   CARBOHYD    206    206
FT   CARBOHYD    208    208
FT   CARBOHYD    210    210
FT   CARBOHYD    222    222
FT   CARBOHYD    227    227       POLYLACTOSAMINOGLYCAN.
FT   CARBOHYD    240    240       POLYLACTOSAMINOGLYCAN.
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    260    260       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    292    292       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    321    321       N-LINKED (GLCNAC. . .).
FT   CONFLICT    379    379       N-LINKED (GLCNAC. . .).
FT   CONFLICT     32     39       VKNGNGTA -> MARGGRVR (IN REF. 3).
SQ   SEQUENCE   416 AA;  44773 MW;  AEED793F7A560CB7 CRC64;

  Query Match          4.6%;  Score 81.5;  DB 1;  Length 416;
  Best Local Similarity   24.3%;  Pred. No. 8.3;
  Matches   34;  Conservative   20;  Mismatches   45;  Indels   41;  Gaps    8;

Qy     204 DPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPH--MENH---------SCFEHMHH 251
           ||:: :     |  | ::||      :| | : | || :   : |         | :
Db      86 DPSLVIAFGRGHTLTLNFT--RNATRYSVQLMSFVYNLSDTHLFPNASSKEIKTVESITD 143

Qy     252 IPAPRPEEFH------QRSNVTLTLRNLKGCCRHQVQIQPFFSS--------CLNDCL 295
           |  |   :::      :|||:||           |    || : |:         |  |
Db     144 IRADIDKKYRCVSGTQVHMNNVTVTL-------HDATIQAYLSNSSFSRGETRCEQD-- 193

Qy     296 RHSATVSCPEMPD-TPEPIP 314
           | | | : |  |  :| |:|
Db     194 RPSPTTAPPAPPSPSPSPVP 213


RESULT  14
Y653_HUMAN
ID   Y653_HUMAN
AC   O75144;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   HYPOTHETICAL PROTEIN KIAA0653 PROTEIN (FRAGMENT)
GN   KIAA0653.
OS   Homo sapiens (Human)
OC   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
```

```
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98403880; PubMed=9734811;
RA   Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA   Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. X.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 5:169-176(1998).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB014553; BAA31628.1; -.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 2.
KW   Hypothetical protein; Glycoprotein; Transmembrane;
KW   Immunoglobulin domain.
FT   NON_TER       1      1
FT   DOMAIN       <1    298       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    299    319       POTENTIAL.
FT   DOMAIN      320    558       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    112    112       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    215    215       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    228    228       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    267    267       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   558 AA;  60890 MW;  63393940F03792F1 CRC64;
```

```
  Query Match             4.6%;  Score 81.5;  DB 1;  Length 558;
  Best Local Similarity   23.0%;  Pred. No. 12;
  Matches   32;  Conservative   13;  Mismatches   57;  Indels   37;  Gaps    5;

Qy     177 SKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTL-WNESTHYQILLT 235
           ||||           |   ||:     :   :      | |:    : |:   |:  |
Db     367 SKNF---------QKAKVPCLEQLLFLETQRSPRWCARHFLQPPLGMGWHPGVHFVTLRW 417

Qy     236 SFPHMENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCL 295
             ||:|       |     : ||     || |    : ::|  ||
Db     418 DFPNM-------HRSRETSARP----PRSPVPSPDQGVQGGSRH---------------- 450

Qy     296 RHSATVSCPEMPDTPEPIP 314
           |  | : |||    | | |
Db     451 RRPAPMGCPEWVQAPAPSP 469
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RESULT  15
RPB3_HUMAN
ID   RPB3_HUMAN     STANDARD;      PRT;   275 AA.
AC   P19387; O15161;
DT   01-NOV-1990 (Rel. 16, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   DNA-DIRECTED RNA POLYMERASE II 33 KDA POLYPEPTIDE (EC 2.7.7.6) (RPB3)
DE   (RNA POLYMERASE II SUBUNIT 3) (RPB33) (RPB31).
GN   POLR2C OR A-152E5.7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90256750; PubMed=2187864;
RA   Pati U.K., Weissman S.M.;
RT   "The amino acid sequence of the human RNA polymerase II 33-kDa
RT   subunit hRPB 33 is highly conserved among eukaryotes.";
RL   J. Biol. Chem. 265:8400-8403(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98201707; PubMed=9540830;
RA   Dammann R., Pfeifer G.P.;
RT   "Cloning and characterization of the human RNA polymerase I subunit
RT   hRPA40.";
RL   Biochim. Biophys. Acta 1396:153-157(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Bruno T., di Padova M., de Angelis R., Iacobini C., Lovari S.,
RA   Passananti C., Fanciulli M.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99425270; PubMed=10493829;
RA   Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
RA   Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA   Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA   Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT   "Genome duplications and other features in 12 Mb of DNA sequence from
RT   human chromosome 16p and 16q.";
RL   Genomics 60:295-308(1999).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC       RNA(N).
CC   -!- SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
CC       POLR2J AND POLR2C SUBUNITS INTERACT WITH EACH OTHER.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC       FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC       PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC       III FOR 5S AND TRNA GENES.
CC   -!- SIMILARITY: BELONGS TO THE RPB3/RPC5 RNA POLYMERASE SUBUNIT
CC       FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J05448; AAA36586.1; -.
DR   EMBL; AF008443; AAC14355.1; -.
DR   EMBL; AJ224143; CAA11842.1; -.
DR   EMBL; AJ224144; CAA11843.1; -.
DR   EMBL; AC004382; AAC24309.1; -.
DR   PIR; A36264; A36264.
DR   MIM; 180663; -.
DR   InterPro; IPR001514; -.
DR   PROSITE; PS00446; RNA_POL_D_30KD; 1.
KW   Transferase; DNA-directed RNA polymerase; Transcription;
KW   Nuclear protein.
FT   DOMAIN       88     97       CYS-RICH.
FT   CONFLICT    194    194       H -> T (IN REF. 1 AND 3).
SQ   SEQUENCE   275 AA;  31441 MW;  EF663BE096046A4B CRC64;
```

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  Query Match             4.6%;  Score 81;  DB 1;  Length 275;
  Best Local Similarity   20.3%;  Pred. No. 5.5;
  Matches   44;  Conservative   28;  Mismatches   81;  Indels   64;  Gaps    8;

Qy      54 NSTCLDDSWI-HPRNLTPSSPKDLQIQLHFAHTQQGDLF-PVAHIEWTLQ---------- 101
```

```
          ||: | | :| |   | |    |:  :| ::     : | |   :|:||
Db     55 NSSVLHDEFIAHRLGLIPLISDDIVDKLQYSRDCTCEEFCPECSVEFTLDVRCNEDQTRH 114

Qy    102 -TDASIL--------------------YLEGAELSVLQLNTNERLCVRFEFLSKLRHHHR 140
           |   ::                    |:|  :: :::|   : | :|          |
Db    115 VTSRDLISNSPRVIPVTSRNRDNDPNDYVEQDDILIVKLRKGQELRLRAYAKKGFGKEHA 174

Qy    141 RWRFTFS-HFVVDPDQEYEVTVHHLPKPIPDG--------------DPNHQSKNFL--VP 183
          :|  |    |  |||     ||:  |:  |                 ||| : : |   |
Db    175 KWNPTAGVAFEYDPDNALRHTVYPKPEEWPKSEYSELDEDESQAPYDPNGKPERFYYNVE 234

Qy    184 DCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVS 220
          |             |||    | :  |   : ::|
Db    235 SC--------------GSLRPETIVLSALSGLKKKLS 257


Search completed: July 17, 2001, 11:21:05
Job time: 159 sec
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Tue Jul 17 11:27:36 2001

us-09-488-728-4_copy_1_320.rpr

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:19:56 ; Search time 26.59 Seconds
(without alignments)
916.730 Million cell updates/sec

Title: US-09-488-728-4_COPY_1_320
Perfect score: 1764
Sequence: 1 MGAARSPPSAVPGPLLGLLL.....VSCPEMPDTPEPIPDYMPLW 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	92	5.2	593	2	H84779	hypothetical prote
2	90.5	5.1	260	2	I51544	MHC class II beta-
3	88.5	5.0	249	1	VGXRHB	glycoprotein VP7 p
4	88.5	5.0	1144	2	A54810	TMV resistance pro
5	88.5	5.0	1402	2	S42748	finger protein - f
6	88	5.0	679	2	B96599	protein F20N2.12 [
7	88	5.0	1210	1	GQHUE	epidermal growth f
8	87.5	5.0	234	2	T45709	hypothetical prote
9	87.5	5.0	1714	1	S18644	multifunctional am
10	86.5	4.9	771	2	JC7388	M83 protein - huma
11	86	4.9	439	1	ISHIX	xylose isomerase (
12	86	4.9	603	2	S03020	dopamine beta-mono
13	85.5	4.8	397	2	JE0082	GPI-linked recepto
14	85	4.8	607	2	S62556	probable serine/th
15	84.5	4.8	1151	2	T38424	hypothetical prote
16	84.5	4.8	1442	2	S72441	protein-tyrosine-p
17	84.5	4.8	1956	2	T00051	hypothetical prote
18	84	4.8	275	2	A36264	DNA-directed RNA p
19	83	4.7	191	2	S57642	interferon precurs
20	83	4.7	275	2	JC6181	RNA polymerase II
21	83	4.7	342	2	T48257	hypothetical prote
22	83	4.7	373	2	S54545	hypothetical prote
23	83	4.7	593	2	T19832	hypothetical prote
24	83	4.7	656	2	T21178	phosphoribosylform
25	83	4.7	741	1	JC1290	conserved hypothet
26	83	4.7	1207	2	C70013	protein-tyrosine k
27	82.5	4.7	540	1	TVFVEB	kinase-related tra
28	82.5	4.7	545	2	S00727	hypothetical prote
29	82.5	4.7	583	2	T30131	hypothetical prote
30	82.5	4.7	959	2	T25704	hypothetical prote
31	82.5	4.7	2025	2	D86201	protein F12K11.6 [
32	82	4.6	448	2	S03186	Ig heavy chain C r
33	81.5	4.6	288	2	C96662	hypothetical prote
34	81.5	4.6	416	1	A31959	lysosome-associate
35	81.5	4.6	1785	2	T21558	hypothetical prote
36	81.5	4.6	1929	2	T21559	hypothetical prote
37	81	4.6	329	2	S77336	pol polyprotein -
38	81	4.6	752	2	D40899	RNA-directed RNA p
39	81	4.6	2244	2	T08212	sugar hydrolase [i
40	80.5	4.6	717	2	E86812	DNA polymerase III
41	80.5	4.6	1164	2	G82100	sensor protein evg
42	80.5	4.6	1197	1	G65010	hypothetical prote
43	80.5	4.6	1227	2	A86245	pyochelin syntheta
44	80.5	4.6	1809	2	T17403	pyochelin syntheta
45	80.5	4.6	1809	2	C83118	

ALIGNMENTS

RESULT 1
H84779
hypothetical protein At2g36370 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84779
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: H84779
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-593 <STO>
A;Cross-references: GB:AE002093; NID:g6598633; PIDN:AAF18663.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g36370
A;Map position: 2

Query Match 5.2%; Score 92; DB 2; Length 593;
Best Local Similarity 22.6%; Pred. No. 6.8;
Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15;

```
Qy      55 STCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDAS-ILYLEGAE 113
           ||||  ||        ||   | |::::|                        |: | || | |
Db     182 STCLVDS------LTDGPPTDVRVRL--------------------TEYSEILDLSGCP 214

Qy     114 LSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDP--DQEYEVTVHHLPKPIPDG 171
           |||   |      |      : ||| :   |: :|  |: ::  : |   ||
Db     215 ----QLNEASLL---LSILPNSYFANLRWRKSLESFLKNPDDDERHQEQISHRTLPILSF 267

Qy     172 DPNHQSKNFLVPDCEHARMKVTTPCMSSG--------SLWDPNITVETLEAHQLRVSFTL 223
           :    |  :  |:    ||   | |                : :  || | ||   :| ::|
Db     268 E---SVKEIDISKCQRLDYKVVIKCFSKSFPSLRKLRAAYLLNIKVSTL--LELLLNFRE 322

Qy     224 WNE----------------STHY--QILLTSF----------------PHMENHSCFEHMH 250
           |                  |  |  |:  |||                ||: :|   ::
Db     323 LTEVDLTVDVSPIIPVQASVFYSGQVCYTSFSENSILALCATISMTNEHMDINSVASNLQ 382

Qy     251 HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMP 307
           :   : |  : | : |   :           |  | || |  : | :| | | |
Db     383 TLHMSKCEGISETSLLNLITHS----------QKMKSLCLRD-TKVSDSVLC-EFP 426
```

RESULT 2
I51544
MHC class II beta-chain - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000

```
C;Accession: I51544
R;Sato, K.; Flajnik, M.F.; Pasquier, L.D.; Katagiri, M.; Kasahara, M.
J. Immunol. 150, 2831-2843, 1992
A;Title: Evolution of the MHC: isolation of class II beta-chain cDNA clones from the Amp
A;Reference number: I51539; MUID:93203604
A;Accession: I51544
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-260 <SAT>
A;Cross-references: GB:D13688; NID:g287582; PIDN:BAA02845.1; PID:g287583
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
F;130-195/Domain: immunoglobulin homology <IMM>


  Query Match                 5.1%;  Score 90.5;  DB 2;  Length 260;
  Best Local Similarity   22.7%;  Pred. No. 3.3;
  Matches   64;  Conservative   34;  Mismatches   97;  Indels   87;  Gaps   17;

Qy      11 VPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLN--------CTVKNSTCLDDS- 61
           :| |:|  ||| ||:                :|| |  :          |  :| |   |:
Db       4 IPVPVL-CLLLTLGL--------------CLCSSPPEDFVYQFKGQCYYRNGT---DNV 44

Qy      62 ---WIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQ 118
             | |  ||  :   |  : |  | |: |   | |   |  | |    :||    :|
Db      45 RLLWRHYYNLEETDYFDSDVGLFIAKTELGK--PDAD-NWNSQKD----FLEQTRAAV-- 95

Qy     119 LNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSK 178
           : :|          ||:::                |: | :                || :
Db      96 ----DTVC---------RHNYQ-----------IDKPYTID--------RKSQPNVKIV 122

Qy     179 NFLVPDCEHARMKVTTPCMSSGSLWDPNITVETL-----EAHQLRVSFTLWNESTHYQI- 232
           |    | ||  :     |   | : | | |  |     |  |: |  | |     ::|
Db     123 NTKTLDLEHENL---ITCFVDG-FFPPMIKVTWLKNGIEEGEQVTSSELLQNGDWTFEIH 178

Qy     233 --LLTSFPHMENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRN 272
             | |:  | :  :|   : |    :|    :  :|: : ||
Db     179 VMLETTIKHGDTFTC--RVEHSSLQQPVSVNWEPDVSESARN 218


RESULT   3
VGXRHB
glycoprotein VP7 precursor - human rotavirus B
C;Species: human rotavirus B
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A37080
R;Chen, G.M.; Hung, T.; Mackow, E.R.
Virology 178, 311-315, 1990
A;Title: Identification of the gene encoding the group B rotavirus VP7 equivalent: prima
A;Reference number: A37080; MUID:90357782
A;Accession: A37080
A;Molecule type: genomic RNA
A;Residues: 1-249 <CHE>
A;Cross-references: EMBL:M33872; NID:g210569; PIDN:AAA42675.1; PID:g210570
A;Note: the authors translated the codon GAT for residue 88 as Val and GTA for residue 8
C;Genetics:
A;Map position: segment 9
C;Superfamily: rotavirus B glycoprotein VP7
C;Keywords: capsid protein; glycoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-249/Product: glycoprotein VP7 #status predicted <VP7>
F;45,91,105/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match                 5.0%;  Score 88.5;  DB 1;  Length 249;
  Best Local Similarity   22.1%;  Pred. No. 4.6;
  Matches   48;  Conservative   30;  Mismatches   82;  Indels   57;  Gaps    9;

Qy     104 ASILYLEGAELSVLQLN----TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEV 159
           ||:| |  |     |||    |:  :|| :                          | |
Db       2 ASLLLLVLAAAVTAQLNIVPSTHPEVCVLY-------------------ADDHQ---- 36

Qy     160 TVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMS-SGSLWDPNITVETLEAHQLR 218
                 | |  : ||      |:   :|   || | | :|    :: :  : |
Db      37 ----------ADANKFNGNF--TQIFHSYNSITLSFMSYSSSSYD---VIDIISKYDLS 80

Qy     219 ----VSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLK 274
                 ::  ::| |  : : | |  :   ::     :||:  || ||:   |      :|||
Db      81 SCNILAIDVFNASMDFNVFLQSTNNCSKYNA-NKVHHVKLPRGEEWFSYS------KNLK 133

Qy     275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPE 311
           |      |  :  : |:|     :|     |: | ||
Db     134 FCPLSDSLIGMYCDTQLSDTYFEISTGGTYEVTDIPE 170


RESULT   4
A54810
TMV resistance protein N - tobacco (Nicotiana glutinosa)
C;Species: Nicotiana glutinosa
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C;Accession: A54810
R;Whitham, S.; Dinesh-Kumar, S.P.; Choi, D.; Hehl, R.; Corr, C.; Baker, B.
Cell 78, 1101-1115, 1994
A;Title: The product of the tobacco mosaic virus resistance gene N: similarity to tol
A;Reference number: A54810; MUID:95007759
A;Accession: A54810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1144 <WHI>
A;Cross-references: GB:U15605; NID:g558886; PIDN:AAA50763.1; PID:g558887
C;Genetics:
A;Gene: N
A;Introns: 160/2; 525/3; 616/3 1139/3


  Query Match                 5.0%;  Score 88.5;  DB 2;  Length 1144;
  Best Local Similarity   20.7%;  Pred. No. 30;
  Matches   44;  Conservative   29;  Mismatches   57;  Indels   83;  Gaps   12;

Qy     172 DPNHQSKNFLVPDCEHARMKVTTPCMSSGSLW---------DPNITVETLEAHQLRVSFT 222
           ||  :|: :|  : |    |   |  |:  ::|           |  |: ::  :||| |
Db     504 DPGERSRLWLAKEVEEV-MSNNTGTMAMEAIWVSSYSSTLRFSNQAVKNMK--RLRV-FN 559

Qy     223 LWNESTHYQI----------LLTSFP-------------HME-NHSCFEHM----HHIP 253
           :   |||| |           : |::|      .       |:  |:   |:     |:|
Db     560 MGRSSTHYAIDYLPNNLRCFVCTNYPWESFPSTFELKMLVHLQLRHNSLRHLWTETKHLP 619

Qy     254 APRPEEFHQRSNVTLT-----LRNLK----------------GCCRHQVQIQPFFSSCL 291
           : |  :      :| |     : ||:                |||   : :      |
Db     620 SLRRIDLSWSKRLTRTPDFTGMPNLEYVNLYQCSNLEEVHHSLGCCSKVIGLY------L 673

Qy     292 NDC-------------LRHSATVSCPEMPDTPE 311
           |||             | :    ||  :   ||
Db     674 NDCKSLKRFPCVNVESLEYLGLRSCDSLEKLPE 706


RESULT   5
S42748
finger protein - fruit fly (Drosophila virilis) (fragment)
C;Species: Drosophila virilis
C;Date: 20-Oct-1994 #sequence_revision 26-May-1995 #text_change 24-Sep-1998
C;Accession: S42748
R;Schuh, R.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42748
A;Accession: S42748
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1402 <SCH>
A;Cross-references: EMBL:Z27444; NID:g426461; PID:g426462
C;Genetics:
A;Gene: FlyBase:Dvir/salm
A;Cross-references: FlyBase:FBgn0013137
C;Keywords: DNA binding; transcription regulation


  Query Match                 5.0%;  Score 88.5;  DB 2;  Length 1402;
```

Best Local Similarity 21.1%; Pred. No. 38;
Matches 74; Conservative 33; Mismatches 114; Indels 129; Gaps 18;

```
Qy       1 MGAARSPPSAVPGPLLGL------LLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKN 54
Db     542 MSFASSP--AFPG-LPGIYRPPMELLKSLGATAGSTAGL----PHPFFPQMPGLGAALKH 594
Qy      55 STCLDDSWIHPRNLT----PSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLE 110
Db     595 TH--DQSQDMPTDLRKSSGPSSPHEEEDNIAARLPVKSELMEEEKTEHTMEAATR----E 648
Qy     111 GAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEY---------EVTV 161
Db     649 SAEMEPLPL-------------EVRIKEER---------IDEDQMHLQEGMQKPEPLTA 685
Qy     162 HHLPKP----IPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQL 217
Db     686 YATPHPQQCLIPTTHAAAKSPRSLPLQC-HARL----------SLW---------------- 720
Qy     218 RVSFTLWNESTHYQILLTSFPHMENHSCF------EHMHHIPAP---------RPEEFHQ 262
Db     721 -----------------CSHPTTSNHACAVLTGSQTHLDQLPTPDNVPPTMPQREDFFAE 763
Db     764 RFPLNFTSKTDDHSPIRSPAGHAHAHIPRSPFFNP-----IKHEMAAFVP 808
```

RESULT 6
B96599
protein F20N2.12 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96599
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Gi
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: B96599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-679 <STO>
A;Cross-references: GB:AE005173; NID:g8778489; PIDN:AAF79497.1; GSPDB:GN00141
C;Genetics:
A;Gene: F20N2.12
A;Map position: 1

Query Match 5.0%; Score 88; DB 2; Length 679;
Best Local Similarity 23.3%; Pred. No. 17;
Matches 80; Conservative 31; Mismatches 116; Indels 116; Gaps 22;

```
Qy      43 CSQPGL-----NCTV----KNSTCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPV 93
Db     200 CCQTNLQEVYYHCSICKFNLNLTC-------ARNPPLSTISHLK-----SHEHPLSIFP- 246
Qy      94 AHIEWTLQTDASILYLEGAELSVLQLNTNERL------------CVRFEFLSKL-RHHH 139
Db     247 --RRIPLPCDACGLSLE---------NTNDYVYACLSCNLMVHMACIFLPRVIKITRHQH 295
Qy     140 RRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
Db     296 ---RLSLSPSL--PSGIYPCGVCRLTIDVTYGQFSCNR------GCHYA---VHSKCAIE 341
Qy     200 GSLWD----------PNITVETLE------------AHQLRVSF--------------- 221
```

```
Db     342 ERIWDGKDLDGVPEEPDEDVEPFERIDDKTIQHFSHEHYLRLNIRNGVFDADSFCQACII 401
Qy     222 -TLWNES----THYQILL----TSFPHMENHSCFEH---MHHIPAPRPEEFHQR-SNVTL 268
Db     402 PILESESFYGCTQCSFLLHEACASFPRKKDHPLHKHRLILHPIP-PKPLEVHMRMMGGKL 460
Qy     269 TLRNLKGC--CRHQVQIQ-PFFSSCLNDCLRHSATVSCPEMPD 308
Db     461 YSRNVKGMFNCSGCDQLGFGFMYICSEKGCRFQLDARCASLPD 503
```

RESULT 7
GQHUE
epidermal growth factor receptor precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999
C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143;
R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.
rg, P.H.
Nature 309, 418-425, 1984
A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression
A;Reference number: A00641; MUID:84219729
A;Accession: A00641
A;Molecule type: mRNA
A;Residues: 1-1210 <ULL>
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
R;Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the human epidermal
A;Reference number: A25772; MUID:85270438
A;Accession: A25772
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <ISH>
A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identificatio
A;Reference number: S30024; MUID:88217333
A;Accession: S30024
A;Molecule type: DNA
A;Residues: 1-29 <HA2>
A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R;Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and premature transcript termi
A;Reference number: A38672; MUID:91107677
A;Accession: A38672
A;Molecule type: DNA
A;Residues: 1-29 <HAL>
A;Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A;Experimental source: carcinoma cell line A431-7
R;Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.;
Nature 309, 806-810, 1984
A;Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RN
A;Reference number: A00642; MUID:84245835
A;Accession: A00642
A;Molecule type: mRNA
A;Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-
',798-799,'TD',802-811,'R',813-942 <XUY>
A;Experimental source: A431 human carcinoma cells, which have large numbers of EGF re
R;Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma,
Science 224, 843-848, 1984
A;Title: Expression cloning of human EGF receptor complementary DNA: gene amplificati
A;Reference number: A43615; MUID:84196372
A;Accession: A43615
A;Molecule type: mRNA
A;Residues: 713-964 <LIN>
A;Experimental source: epidermoid carcinoma cell line A431
R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
```
```

```
A;Reference number: A23062; MUID:85046483
A;Accession: A23062
A;Molecule type: mRNA
A;Residues: 1028-1210 <SIM>
R;Weber, W.; Gill, G.N.; Speiss, J.
Science 224, 294-297, 1984
A;Reference number: A05281; MUID:84172183
A;Accession: A05281
A;Molecule type: protein
A;Residues: 25-30,'S',32-51;454-467 <WEB>
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A;Title: Identification of residues in the nucleotide binding site of the epidermal grow
A;Reference number: A60143; MUID:85182650
A;Accession: A60143
A;Molecule type: protein
A;Residues: 740-744,'X',746-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A;Title: ATP-stimulated interaction between epidermal growth factor receptor and supercc
A;Reference number: A38023; MUID:84191554
A;Contents: annotation; receptor activity
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.
Cell 59, 33-43, 1989
A;Title: Functional independence of the epidermal growth factor receptor from a domain r
A;Reference number: A33331; MUID:90003233
A;Contents: annotation; internalization signal
C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor c
C;Genetics:
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Map position: 7p12.3-7p12.1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1210/Product: EGF receptor #status predicted <MAT>
F;25-645/Domain: extracellular #status predicted <EXT>
F;75-300/Domain: EGF receptor extracellular domain repeat <EE1>
F;390-600/Domain: EGF receptor extracellular domain repeat <EE2>
F;646-668/Domain: transmembrane #status predicted <TMM>
F;669-1210/Domain: intracellular #status predicted <INT>
F;710-975/Domain: protein kinase homology <KIN>
F;718-726/Region: protein kinase ATP-binding motif
F;999-1046/Region: coated-pit mediated internalization signal
F;1047-1210/Region: inhibitory
F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predic
F;745/Active site: Lys #status experimental

  Query Match             5.0%;  Score 88;  DB 1;  Length 1210;
  Best Local Similarity   22.6%;  Pred. No. 35;
  Matches   93;  Conservative   45;  Mismatches  156;  Indels  118;  Gaps   22;

Qy      15 LLGLLLL----LLGVLAPGGASLRLL-DHRALVCSQPGLNCTV---KNSTCLDD-SWIH- 64
           |||: |     |:  | | |  |  : :|:  : ||  ||  |   |    |:|   :|
Db     777 LLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRRLVHR 836

Qy      65 ---PRNLTPSSPKDLQIQ-----------------------------LHFAHTQQGD 89
             ||:   :|: ::|                                 ||  :| | |
Db     837 DLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALESILHRIYTHQSD 896

Qy      90 LFPVAHIEWTLQTDASILY--LEGAELSVLQLNTNERL-----CVRFEFL---------S 133
           ::       | | |  |  |  :  :|:| : |   |||     |    ::         :
Db     897 VWSYGVTVWELMTFGSKPYDGIPASEISSI-LEKGERLPQPPICTIDVYMIMVKCWMIDA 955

Qy     134 KLRHHHRRWRFTFSHFVVDPDQEYEVTV----HHLPKPI-----------PDGDPNHQSK 178
           |   |    ||    || | | |           |||  |            | |    :
Db     956 DSRPKFRELIIEFSKMARDP-QRYLVIQGDERMHLPSPTDSNFYRALMDEEDMDDVVDAD 1014

Qy     179 NFLVPDCEHARMKVT--TPCMSSGSLWDPNITVETLEAHQLRV------SF--------- 221
           :|:|          |  || :|| |     | ||  :: : |:       ||
Db    1015 EYLIPQQGFFSSPSTSRTPLLSSLSATSNNSTVACIDRNGLQSCPIKEDSFLQRYSSDPT 1074

Qy     222 -TLWNESTHYQILLT------SFPHMENHSCFEHMHH----IPAPRPEEFHQRSNVTLTL 270
            |  :|     |        | |     |    ::|      |||  :  :|  : |
Db    1075 GALTEDSIDDTFLPVPEYINQSVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAV- 1133

Qy     271 RNLKGCCRHQVQIQPFFSSCLN---DCLRHSATVSCPEMP-DTPEPIPDYMP 318
                 |  :  :||   :|:|   |   | |        ::  | |:   |: |
Db    1134 ----GNPEYLNTVQP---TCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFP 1178


RESULT   8
T45709
hypothetical protein F1P2.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45709
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.,
submitted to the Protein Sequence Database, November 1999
A;Reference number: Z23010
A;Accession: T45709
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <CHO>
A;Cross-references: EMBL:AL132955
A;Experimental source: cultivar Columbia; BAC clone F1P2
C;Genetics:
A;Map position: 3
A;Introns: 166/3; 179/3; 208/1
A;Note: F1P2.40

  Query Match             5.0%;  Score 87.5;  DB 2;  Length 234;
  Best Local Similarity   22.8%;  Pred. No. 5.1;
  Matches   44;  Conservative   20;  Mismatches   82;  Indels   47;  Gaps    9;

Qy     122 NERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFL 181
           : |:|    |  || |              :  :| |       |    ||    ||  :   |
Db      10 SRRICNLLIFFVKLNH---------KNLSIDSDNPQ----HSAMKP----DPTRRRNRAL 52

Qy     182 VPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILL------- 234
                :   | | :||||   ||          ::: | || :     :: |
Db      53 ----SSSSPSKTRPELSSGS---PNRNTGEARGGKVKTSATLLDRE---EMGLFPGSGYG 102

Qy     235 ------TSFPHMENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGC----CRHQVQIQ 284
                 |||:      |:|    |   || : :     :  | | ||    |     |
Db     103 DPNPEPRSFPYSVKQQCWEKAEKIKGRDPERWRRDHLGNIVFRKLVGCPGCLCHDYDHIV 162

Qy     285 PFF---SSCLNDC 294
           |:     | | :|
Db     163 PYSKGGKSTLENC 175


RESULT   9
S18644
multifunctional amino acid--tRNA ligase (EC 6.1.1.-) - fruit fly (Drosophila melanoga
N;Alternate names: multifunctional aminoacyl-tRNA synthetase
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S18644
R;Cerini, C.; Kerjan, P.; Astier, M.; Gratecos, D.; Mirande, M.; Semeriva, M.
EMBO J. 10, 4267-4277, 1991
A;Title: A component of the multisynthetase complex is a multifunctional aminoacyl-tR
A;Reference number: S18644; MUID:92097547
A;Accession: S18644
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1714 <CER>
A;Cross-references: GB:M74104; NID:g157563; PIDN:AAA28594.1; PID:g157564
C;Genetics:
A;Gene: FlyBase:Aats-glupro
A;Cross-references: FlyBase:FBgn0005674
C;Superfamily: Drosophila multifunctional amino acid--tRNA ligase; amino acid--tRNA l
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; multifunctional enzyme; protein b
```

F;204-480/Domain: glutamine--tRNA ligase homology <EGL>
F;755-800/Domain: amino acid--tRNA ligase repeat homology <ATL1>
F;827-872/Domain: amino acid--tRNA ligase repeat homology <ATL2>
F;901-946/Domain: amino acid--tRNA ligase repeat homology <ATL3>
F;980-1025/Domain: amino acid--tRNA ligase repeat homology <ATL4>
F;1055-1100/Domain: amino acid--tRNA ligase repeat homology <ATL5>
F;1129-1173/Domain: amino acid--tRNA ligase repeat homology <ATL6>

Query Match 5.0%; Score 87.5; DB 1; Length 1714;
Best Local Similarity 19.2%; Pred. No. 59;
Matches 71; Conservative 48; Mismatches 119; Indels 131; Gaps 17;

```
Qy      32 SLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSP----------KDLQIQ-- 79
Db      39 SLQFPDNRLLVCH--------SNNDVL-------RALARAAPDYKLYGETAIERTQIDHW 83
Qy      80 LHFAHTQQGDLFPVAHIEWTLQTDAS----ILYLEGAELSVLQLNTNERLCVRFEFLSK- 134
Db      84 LSFSLTCEDD------ISWALSFLTSPLPPVTYLVANKLTIADFALFNEMHSRYEFLAAK 137
Qy     135 -LRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPK--------------PIPDGDPNHQSK 178
Db     138 GIPQHVQRW-----YDLITAQPLIQKVLQSLPEDAKVKRSPQSSKEQTPAKTGERKQEGK 192
Qy     179 NFLVPDCEHARMKVTTPCMSSGSLW------------------------DPNITVETL 212
Db     193 FVDLPGAEMGKVVVRFPPEASGYLHIGHAKAALLNQYYALVCQGTLIMRFDDTNPAKETV 252
Qy     213 E--------AHQLRVSFTLWNESTHYQILLTSFPHMENHSCF----EHMHHIPAPRPE-- 258
Db     253 EFENVILGDLEQLQIKPDVFTHTSNYFDLMLDY-------CVRLIKESKAYVDDTPPEQM 305
Qy     259 --EFHQR----------SNVTLTLRNLKG-------CCRHQVQIQPFFSSCLNDCLRHS 298
Db     306 KLEREQRVESANRSNSVEKNLSLWEEMVKGSEKGQNTACAAKIDM-----SSPNGCMRDP 360
Qy     299 ATVSCPEMP 307
Db     361 TIYRCKNEP 369
```

RESULT 10
JC7388
M83 protein - human
C;Species: Homo sapiens (man)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 01-Dec-2000
C;Accession: JC7388
R;Motohashi, T.; Miyoshi, S.; Osawa, M.; Eyre, H.J.; Sutherland, G.R.; Matsuda, Y.; Naka
Biochem. Biophys. Res. Commun. 276, 244-250, 2000
A;Title: Molecular cloning and chromosomal mapping of a novel five-span transmembrane pr
A;Reference number: JC7388
A;Accession: JC7388
A;Molecule type: mRNA
A;Residues: 1-771 <MOT>
A;Cross-references: DDBJ:AB045292
C;Comment: This protein, as a glycosylated cell surface protein, which belongs to a new
 Its biological role is related to the T cell resting status.
C;Genetics:
A;Gene: m83
A;Map position: 16p13.3L
C;Keywords: extracellular protein; glycolysis; transmembrane protein

Query Match 4.9%; Score 86.5; DB 2; Length 771;
Best Local Similarity 21.1%; Pred. No. 27;
Matches 75; Conservative 35; Mismatches 118; Indels 127; Gaps 15;

```
Qy       5 RSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIH 64
Db      71 RVPPDAV------LLRWLLQVSRESGAA----------------CTDAEIT------VH 101
Qy      65 PRNLTP--------SSPKDLQIQLHF----------------AHTQQGDLFPVAHIEW 98
```

```
Db     102 FRSGAPPVINPLGTSFPDDTAVQPSFQVGVPLSTAPRSNASVNVSHPAPGDWFVAAH--- 158
Qy      99 TLQTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYE 158
Db     159 -LPPSSQKIELKGLAPTCAYVFQPELLVTRVVEIS----------------IMEPD---- 197
Qy     159 VTVHHLPKPIPDGDPNHQS-KNFLVPDCEHARMKVTTPCMSSGSLWDP-NITV--ETLEA 214
Db     198 -------VPLPQTLLSHPSYLKVFVPDYTRELLLELRDCVSNGSLGCPVRLTVGPVTLPS 250
Qy     215 HQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAPRPEEFHQRSNVTL------ 268
Db     251 NFQKV-LTCTGAPWPCRLLL----------------PSPPWDRWLQVTAESLVGPLGT 291
Qy     269 ----TLRNLKGCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPL 319
Db     292 VAFSAVAALTACRPRSVTVQPLLQSSQNQSFNASSGLLSPS--------PDHQDL 338
```

RESULT 11
ISHIX
xylose isomerase (EC 5.3.1.5) - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 06-Dec-1996 #text_change 18-Jun-1999
C;Accession: D64183
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
A;Accession: D64183
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-439 <TIGR>
A;Cross-references: GB:U32791; GB:L42023; NID:g1574662; PIDN:AAC22766.1; PID:g1574666
C;Genetics:
A;Gene: xylA
A;Map position: FOR1177317-1178636
C;Function:
A;Description: catalyzes isomerization of the aldopentose D-xylose to the 2-ketopento
A;Pathway: xylose metabolism
C;Superfamily: xylose isomerase
C;Keywords: intramolecular oxidoreductase; isomerase; magnesium; xylose metabolism
F;101,104/Active site: His, Asp #status predicted
F;141,234/Binding site: substrate (Thr, Lys) #status predicted
F;232,268,296,339/Binding site: magnesium (Glu, Glu, Asp, Asp) #status predicted
F;268,271,307,309/Binding site: magnesium (Glu, His, Asp, Asp) #status predicted

Query Match 4.9%; Score 86; DB 1; Length 439;
Best Local Similarity 20.6%; Pred. No. 15;
Matches 47; Conservative 34; Mismatches 71; Indels 76; Gaps 10;

```
Qy      76 LQIQLHFAHT---QQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLNTNERLCVRFEFL 132
Db      42 LRLAVCYWHTFCWNGNDMFGLGSLERSWQKNSNL--LAGAE---------QKADIAFEFL 90
Qy     133 SKLRHHHRRWRFTFSHFVVDPD----QEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHA 188
Db      91 NKLGVPY----YCFHDVDIAPEGNSVREYVQNFHH----------------IVDILERK 129
Qy     189 RMKV------------TTPCMSSGSLWDPNITVETLEAHQL-----------RVSFTLWN 225
Db     130 QVETGVKLLWGTANCFTNPRYMSGAATNPNPEVFAWAATQVFNAMNATQRLGGENYVLWG 189
Qy     226 ESTHYQILLTSFPHMENHS-------CFEHMHHIP-------APRPEE 259
Db     190 GREGYETLLNTDLKRREREQIGRFMQMVVEHKHKIGFKGTLLIEPKPQE 237
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RESULT  12
S03020
dopamine beta-monooxygenase (EC 1.14.17.1) precursor - human
N;Alternate names: dopamine beta-hydroxylase
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
C;Accession: S03020; S06283; S61362; I37276
R;Kobayashi, K.; Kurosawa, Y.; Fujita, K.; Nagatsu, T.
Nucleic Acids Res. 17, 1089-1102, 1989
A;Title: Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-termin
A;Reference number: S03020; MUID:89160241
A;Accession: S03020
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-603 <KOB>
A;Cross-references: EMBL:X13255; NID:g30473; PIDN:CAA31631.1; PID:g30474
A;Note: 304-Ser and 535-Cys were also found; the amino acid exchange at residue 535 was
A;Note: the authors translated the codon TGC for residue 380 as Lys
R;Lamouroux, A.; Vigny, A.; Biguet, N.F.; Darmon, M.C.; Franck, R.; Henry, J.P.; Mallet,
EMBO J. 6, 3931-3937, 1987
A;Title: The primary structure of human dopamine-beta-hydroxylase: insights into the rel
A;Reference number: S06283; MUID:88166633
A;Accession: S06283
A;Molecule type: mRNA
A;Residues: 1-196,'T',198-534,'C',536-603 <LAM>
A;Cross-references: EMBL:Y00096; NID:g30455; PIDN:CAA68285.1; PID:g30456
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: 502-Leu and 507-Gly were also found
R;Li, B.; Tsing, S.; Kosaka, A.H.; Nguyen, B.; Osen, E.G.; Bach, C.; Chan, H.; Barnett,
Biochem. J. 313, 57-64, 1996
A;Title: Expression of human dopamine beta-hydroxylase in Drosophila Schneider 2 cells.
A;Reference number: S61362; MUID:96132606
A;Accession: S61362
A;Molecule type: protein
A;Residues: 26-34 <LIB>
C;Superfamily: peptidylglycine monooxygenase I homology
C;Keywords: catecholamine biosynthesis; copper; glycoprotein; monooxygenase; oxidoreduct
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-603/Product: dopamine beta-hydroxylase #status predicted <MAT>
F;282-505/Domain: peptidylglycine monooxygenase I homology <PGM>

  Query Match                4.9%;  Score 86;  DB 2;  Length 603;
  Best Local Similarity     19.4%;  Pred. No. 22;
  Matches   54;  Conservative   42;  Mismatches  110;  Indels   72;  Gaps   14;

Qy      68 LTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL-------------QTDASILY----- 108
           |  |:|::  :  |      :| |     : | :             :  | :|:
Db      23 LQGSAPRESPLPYHIPLDPEGSL----ELSWNVSYTQEAIHFQLLVRRLKAGVLFGMSDR 78

Qy     109 --LEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYE-VTVHHLP 165
           -|| |:| ||  :             :    |         :|| |:|: : |   |
Db      79 GELENADLVVLWTD-----------GDTAYFADAWSDQKGQIHLDPQQDYQLLQVQRTP 126

Qy     166 --------KPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQL 217
                  :|    ||    |::|: |         |  :  | | :|  ::| :    |
Db     127 EGLTLLFKRPFGTCDP----KDYLIED--------GTVHLVYGILEEPFRSLEAINGSGL 174

Qy     218 RVSFTLWNESTHYQILLTSFPHME--NHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNL-K 274
           ::          |:|  : |   |  : :|      : ||  :    | :     :: | |
Db     175 QMGL------QRVQLLKPNIPEPELPSDAC---TMEVQAPNIQIPSQETTYWCYIKELPK 225

Qy     275 GCCRHQ-VQIQPFFSSCLNDCLRHSATVSC-PEMPDTP 310
           |  ||  :: :|  :      : |     | |||   |
Db     226 GFSRHHIIKYEPIVTKGNEALVHHMEVFQCAPEMDSVP 263


RESULT  13
JE0082
GPI-linked receptor precursor - mouse
N;Alternate names: GFRalpha-3
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 02-Jun-2000
C;Accession: JE0082
R;Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
Biochem. Biophys. Res. Commun. 244, 849-853, 1998
A;Title: Molecular cloning and expression analysis of GFRalpha-3,a novel cDNA related
A;Reference number: JE0082; MUID:98205811
A;Accession: JE0082
A;Molecule type: mRNA
A;Residues: 1-397 <NOM>
A;Cross-references: DDBJ:AB008833; NID:g2627159; PIDN:BAA23562.1; PID:g2627160
C;Comment: This protein plays a distinct role in cell survival and differentiation.
C;Superfamily: Mus musculus GPI-linked receptor
C;Keywords: glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;380-397/Region: hydrophobic
F;92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match                4.8%;  Score 85.5;  DB 2;  Length 397;
  Best Local Similarity     24.7%;  Pred. No. 14;
  Matches   82;  Conservative   28;  Mismatches  123;  Indels   99;  Gaps   19;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALV--CSQPGLNCTVKNSTCL 58
           || : ||      ||| :|||:| :  | ||    |      |  |:|    |   | |
Db       1 MGLSWSPRP----PLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEA-NPAC- 54

Qy      59 DDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQ 118
             :: |  : | |  : | ::                    |  :  |     || ||   |
Db      55 KAAYQHLGSCTSSLSRPLPLE----------------ESAMSADC----LEAAE----Q 89

Qy     119 LNTNERLCVRFEFLSKLRHHHRRWRFTFS----HFVVDP-----DQE-----YEVTVHHL 164
           |  :  : |              ||| :   :   :: | |     | |     || ||
Db      90 LRNSSLIDCRC---------HRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSK 140

Qy     165 PKPIPDGDPNHQSKNFLVPD----------------CEHARMKVTTPCMSSGSLWDPNIT 208
           |  :     |    | | ||                |:  |     |  ||     ::
Db     141 PWKM-----NLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEAC--SGIRCQRHLC 193

Qy     209 VETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAPR---PEEFHQRSN 265
           :        |||  |    || | | ||       |:  | |   :  ||    |      :
Db     194 LA-----QLRSFFEKAAES-HAQGLLLCPCAPEDAGCGERRRNTIAPSCALP-------S 240

Qy     266 VTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRH 297
           ||    :|:  ||      |   | | |   |
Db     241 VTPNCLDLRSFCR----ADPLCRSRLMDFQTH 268


RESULT  14
S62556
probable serine/threonine protein kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
C;Accession: S62556; T38338
R;Odell, C.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S62546
A;Accession: S62556
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-607 <ODE>
A;Cross-references: EMBL:Z67757; NID:g1061288; PIDN:CAA91776.1; PID:g1061299
R;Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21786
A;Accession: T38338
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-607 <OD2>
A;Cross-references: EMBL:Z67757; PIDN:CAA91776.1; GSPDB:GN00066; SPDB:SPAC24B11.11c
A;Experimental source: strain 972h-; cosmid c24B11
C;Genetics:
A;Gene: SPAC24B11.11c
A;Map position: 1L
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
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C;Keywords: ATP
F;206-508/Domain: protein kinase homology <KIN>
F;214-222/Region: protein kinase ATP-binding motif

Query Match 4.8%; Score 85; DB 2; Length 607;
Best Local Similarity 21.7%; Pred. No. 27;
Matches 60; Conservative 30; Mismatches 85; Indels 102; Gaps 14;

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Qy      89 DLFPVAHIEWTLQ-----TDASILYL-----EGAELSVLQLNTNERLCVRFEFLSKLRHH 138
           |:   |: || ::       | | :||      | :   |  |:                 || |
Db     258 DILTTANSEWLVRLLYAFQDTSNIYLAMEFVPGGDFRTLLSNS----------GVLRDH 306

Qy     139 HRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMS 198
           | ::  |     :|        :| |     |  |    :||||    |  :|:|   :|
Db     307 HAKFYATEMFLAID-------ALHQLGYIHRDLKP----ENFLVGASGH--IKLTDFGLS 353

Qy     199 SGSLWDP------------NITVETLEAHQLRVSF-TL-------------------- 223
           || :                |: |      : |  | ||
Db     354 SGIISKKKIESMKIRLQEVNNVVVPERSMRERRQVFRTLLSQDPVYAHSVVGSPDYMAPE 413

Qy     224 ------WNESTHYQIL-------LTSFP-----------HMEN-HSCFEHMHHIPAPRP 257
                :| |   |  |        |: ||           :::|   ||:  |:   ||
Db     414 VLRGENYNHSVDYWSLGCIMYECLSGFPPFSGSNVNETWSNLKNWRKCFQRPHY-DDPRD 472

Qy     258 EEFHQRSNV------TLTLRNLKGCCRHQVQIQPFFS 288
           ||: | :        :|    : |   ||   |:||
Db     473 LEFNWRDDAWDFVCHCITDPKDRFCSLKQVMQHPYFS 509
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RESULT 15
T38424
hypothetical protein SPAC26H5.05, Ank repeat containing - fission yeast (Schizosaccharom
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38424
R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21748
A;Accession: T38424
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1151 <OLI>
A;Cross-references: EMBL:Z99126; PIDN:CAB16191.1; GSPDB:GN00066; SPDB:SPAC26H5.05
A;Experimental source: strain 972h-; cosmid c26H5
C;Genetics:
A;Gene: SPDB:SPAC26H5.05
A;Map position: 1

Query Match 4.8%; Score 84.5; DB 2; Length 1151;
Best Local Similarity 25.1%; Pred. No. 64;
Matches 43; Conservative 28; Mismatches 57; Indels 43; Gaps 10;

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Qy      91 FPVAHI------EWTLQTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRF 144
           | | |:      :|  : : ::|:        |:: :|:   | ||:|      ||  :
Db     232 FSVNHLPAINEHKWKSRVETNMLF-------ELRIKSNDNQSVPFEYLRLPSWAHREDKK 284

Qy     145 TFSH-FVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDC----------EHARMKVT 193
             |   : || |   ||- ||   :  ||     |: :|  |                :|| : |
Db     285 RSSKPQPLQPDPE---TVIHLVPTVLAGD-----KSSVVKTCCTRCLLRERKRNARSQAT 336

Qy     194 -TPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQI-LLTSFPHMEN 242
            ||       || |   |:|::  ::     |   ::| ||  || :|:
Db     337 KDACM-------PNYT--KLKAYERNMTDASPEEKQQFRIKLLNQFPKLED 378
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Job time: 152 sec

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Tue Jul 17 11:27:35 2001

us-09-488-728-4_copy_1_320.rai

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 11:19:22 ; Search time 21.86 Seconds
(without alignments)
294.889 Million cell updates/sec

Title: US-09-488-728-4_COPY_1_320
Perfect score: 1764
Sequence: 1 MGAARSPPSAVPGPLLGLLL.....VSCPEMPDTPEPIPDYMPLW 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1764	100.0	866	2	US-08-620-694A-10	Sequence 10, Appl
2	1764	100.0	866	3	US-09-022-255-10	Sequence 10, Appl
3	1764	100.0	866	3	US-09-022-696-10	Sequence 4, Appli
4	1764	100.0	866	3	US-08-978-773-4	Sequence 10, Appl
5	1764	100.0	866	3	US-09-022-253-10	Sequence 10, Appl
6	1764	100.0	866	3	US-09-022-260-10	Sequence 10, Appl
7	1764	100.0	866	4	US-09-022-259-10	Sequence 10, Appl
8	1764	100.0	866	4	US-09-022-257-10	Sequence 2, Appli
9	1254	71.1	864	2	US-08-620-694A-2	Sequence 2, Appli
10	1254	71.1	864	3	US-09-022-255-2	Sequence 2, Appli
11	1254	71.1	864	3	US-09-022-696-2	Sequence 2, Appli
12	1254	71.1	864	3	US-08-978-773-2	Sequence 2, Appli
13	1254	71.1	864	3	US-09-022-253-2	Sequence 2, Appli
14	1254	71.1	864	3	US-09-022-260-2	Sequence 2, Appli
15	1254	71.1	864	4	US-09-022-259-2	Sequence 2, Appli
16	1254	71.1	864	4	US-09-022-257-2	Sequence 108, App
17	88.5	5.0	1143	2	US-08-310-912A-108	Sequence 108, App
18	88.5	5.0	1143	5	PCT-US95-04589-108	Sequence 2, Appli
19	88.5	5.0	1144	1	US-08-261-663A-2	Sequence 4, Appli
20	88.5	5.0	1144	1	US-08-261-663A-4	Sequence 2, Appli
21	88.5	5.0	1144	5	PCT-US95-07754A-2	Sequence 4, Appli
22	88.5	5.0	1144	5	PCT-US95-07754A-4	Sequence 4, Appli
23	88	5.0	1210	2	US-08-475-035-4	Sequence 7, Appli
24	87	4.9	1210	2	US-08-484-438-7	Sequence 16, Appl
25	84.5	4.8	410	1	US-08-073-807A-16	Sequence 17, Appl
26	81.5	4.6	353	1	US-08-073-807A-17	Sequence 18, Appl
27	81.5	4.6	380	1	US-08-073-807A-18	Sequence 2, Appli
28	81.5	4.6	416	1	US-08-073-807A-2	Sequence 9, Appli
29	81.5	4.6	1144	3	US-08-930-996A-9	Patent No. 5266464
30	79	4.5	671	6	5266464-2	Sequence 8, Appli
31	78.5	4.5	337	5	PCT-US94-14277-8	Sequence 20, Appl
32	78.5	4.5	1213	1	US-08-188-582-20	Sequence 20, Appl
33	78.5	4.5	1213	1	US-08-646-715-20	Sequence 17, Appl
34	77.5	4.4	368	1	US-08-211-942-17	Patent No. 5194375
35	77	4.4	459	6	5194375-2	Sequence 11, Appl
36	76.5	4.3	169	3	US-08-630-172-11	Sequence 3, Appli
37	76.5	4.3	954	2	US-08-749-169A-3	Sequence 3, Appli
38	76.5	4.3	954	2	US-09-130-032A-3	Sequence 2, Appli
39	76	4.3	429	1	US-07-964-589-2	Sequence 2, Appli
40	76	4.3	429	5	PCT-US93-02024-2	Sequence 2, Appli
41	75.5	4.3	1626	2	US-08-771-602D-2	Sequence 2, Appli
42	75.5	4.3	1626	4	US-09-232-446B-2	Sequence 2, Appli
43	75	4.3	839	1	US-08-087-016-2	Sequence 2, Appli
44	74.5	4.2	399	4	US-09-284-033-2	Sequence 2, Appli
45	74.5	4.2	399	4	US-08-729-834B-2	

ALIGNMENTS

RESULT 1
US-08-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-620-694A-10

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  Query Match             100.0%;  Score 1764;  DB 2;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-177;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
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Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
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Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
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Db     301 VSCPEMPDTPEPIPDYMPLW 320


RESULT   2
US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072033el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,255
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/620,694
;      FILING DATE:  21 MARCH 1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
; INFORMATION FOR SEQ ID NO:  10:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-255-10


  Query Match             100.0%;  Score 1764;  DB 3;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-177;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
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Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
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Db     301 VSCPEMPDTPEPIPDYMPLW 320


RESULT   3
US-09-022-696-10
; Sequence 10, Application US/09022696
; Patent No. 6072037
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072037el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,696
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-696-10

Query Match 100.0%; Score 1764; DB 3; Length 866;
Best Local Similarity 100.0%; Pred. No. 8.9e-177;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Qy     301 VSCPEMPDTPEPIPDYMPLW 320
Db     301 VSCPEMPDTPEPIPDYMPLW 320
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RESULT 4
US-08-978-773-4
; Sequence 4, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Troutt, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2623-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-773-4

Query Match 100.0%; Score 1764; DB 3; Length 866;
Best Local Similarity 100.0%; Pred. No. 8.9e-177;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Qy     301 VSCPEMPDTPEPIPDYMPLW 320
Db     301 VSCPEMPDTPEPIPDYMPLW 320
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RESULT 5
US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:

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;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/410,535
;       FILING DATE:  23 MARCH 1995
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Perkins, Patricia Anne
;       REGISTRATION NUMBER:  34,695
;       REFERENCE/DOCKET NUMBER:  2617-B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206)587-0430
;       TELEFAX:  (206)
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  866 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-022-253-10


  Query Match                 100.0%;  Score 1764;  DB 3;  Length 866;
  Best Local Similarity       100.0%;  Pred. No. 8.9e-177;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
Db     301 VSCPEMPDTPEPIPDYMPLW 320


RESULT   6
US-09-022-260-10
; Sequence 10, Application US/09022260
; Patent No. 6100235
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6100235el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
,      ADDRESSEE:  Immunex Corporation
,      STREET:  51 University Street
,      CITY:  Seattle
,      STATE:  WA
,      COUNTRY:  USA
,      ZIP:  98101
,    COMPUTER READABLE FORM:
,      MEDIUM TYPE:  Floppy disk
,      COMPUTER:  Apple Power Macintosh
,      OPERATING SYSTEM:  Apple Operating System 7.5.5
,      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
,    CURRENT APPLICATION DATA:
,      APPLICATION NUMBER:  US/09/022,260
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-260-10


  Query Match                 100.0%;  Score 1764;  DB 3;  Length 866;
  Best Local Similarity       100.0%;  Pred. No. 8.9e-177;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
Db     301 VSCPEMPDTPEPIPDYMPLW 320


RESULT   7
US-09-022-259-10
; Sequence 10, Application US/09022259
; Patent No. 6191104
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6191104el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
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      MEDIUM TYPE:  Floppy disk
      COMPUTER:  Apple Power Macintosh
      OPERATING SYSTEM:  Apple Operating System 7.5.5
      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/022,259
      FILING DATE:
      CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  08/620,694
      FILING DATE:
      CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  USSN 08/410,535
      FILING DATE:  23 MARCH 1995
      CLASSIFICATION:
    ATTORNEY/AGENT INFORMATION:
      NAME:  Perkins, Patricia Anne
      REGISTRATION NUMBER:  34,695
      REFERENCE/DOCKET NUMBER:  2617-B
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (206)587-0430
      TELEFAX:  (206)
    INFORMATION FOR SEQ ID NO:  10:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 866 amino acids
      TYPE:  amino acid
      TOPOLOGY:  linear
    MOLECULE TYPE:  protein
US-09-022-259-10

  Query Match           100.0%;  Score 1764;  DB 4;  Length 866;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-177;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
Db     301 VSCPEMPDTPEPIPDYMPLW 320


RESULT   8
US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6197525el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE   Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
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;      APPLICATION NUMBER:  US/09/022,257
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;    INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-257-10

  Query Match           100.0%;  Score 1764;  DB 4;  Length 866;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-177;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
Db     301 VSCPEMPDTPEPIPDYMPLW 320


RESULT   9
US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
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;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 5869286el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694A
;      FILING DATE:  21 MARCH 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-620-694A-2


  Query Match                 71.1%;  Score 1254;  DB 2;  Length 864;
  Best Local Similarity   71.4%;  Pred. No. 3.8e-123;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
Db       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
Db      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
Db     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
Db     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
Db     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300

Qy     301 VSCPEMPDT--PEPIPDYMPLW 320
Db     301 VPCPVISNTTVPKPVADYIPLW 322
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  ; Sequence 2, Application US/09022255
  ; Patent No. 6072033
  ;  GENERAL INFORMATION:
  ;    APPLICANT:  Yao, Zhengbin
  ;    APPLICANT:  Spriggs, Melanie
  ;    APPLICANT:  Fanslow, William
  ;    TITLE OF INVENTION:  No. 6072033el Receptor That Binds IL-17
  ;    NUMBER OF SEQUENCES:  10
  ;    CORRESPONDENCE ADDRESS:
  ;      ADDRESSEE:  Immunex Corporation
  ;      STREET:  51 University Street
  ;      CITY:  Seattle
  ;      STATE:  WA
  ;      COUNTRY:  USA
  ;      ZIP:  98101
  ;    COMPUTER READABLE FORM:
  ;      MEDIUM TYPE:  Floppy disk
  ;      COMPUTER:  Apple Power Macintosh
  ;      OPERATING SYSTEM:  Apple Operating System 7.5.5
  ;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
  ;    CURRENT APPLICATION DATA:
  ;      APPLICATION NUMBER:  US/09/022,255
  ;      FILING DATE:
  ;      CLASSIFICATION:
  ;    PRIOR APPLICATION DATA:
  ;      APPLICATION NUMBER:  USSN 08/620,694
  ;      FILING DATE:  21 MARCH 1996
  ;      APPLICATION NUMBER:  USSN 08/538,765
  ;      FILING DATE:  7 AUGUST 1995
  ;    PRIOR APPLICATION DATA:
  ;      APPLICATION NUMBER:  USSN 08/410,535
  ;      FILING DATE:  23 MARCH 1995
  ;    ATTORNEY/AGENT INFORMATION:
  ;      NAME:  Perkins, Patricia Anne
  ;      REGISTRATION NUMBER:  34,695
  ;      REFERENCE/DOCKET NUMBER:  2617-B
  ;    TELECOMMUNICATION INFORMATION:
  ;      TELEPHONE:  (206)587-0430
  ;      TELEFAX:  (206)
  ;  INFORMATION FOR SEQ ID NO:  2:
  ;    SEQUENCE CHARACTERISTICS:
  ;     LENGTH: 864 amino acids
  ;      TYPE:  amino acid
  ;      TOPOLOGY:  linear
  ;    MOLECULE TYPE:  protein
  US-09-022-255-2


  Query Match                 71.1%;  Score 1254;  DB 3;  Length 864;
  Best Local Similarity   71.4%;  Pred. No. 3.8e-123;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

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Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
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; Patent No. 6072037
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    APPLICANT:  Spriggs, Melanie
    APPLICANT:  Fanslow, William
    TITLE OF INVENTION:  No. 6072037el Receptor That Binds IL-17
    NUMBER OF SEQUENCES:  10
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Immunex Corporation
      STREET:  51 University Street
      CITY:  Seattle
      STATE:  WA
      COUNTRY:  USA
      ZIP:  98101
    COMPUTER READABLE FORM:
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      COMPUTER:  Apple Power Macintosh
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      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
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      FILING DATE:
      CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  USSN 08/410,535
      FILING DATE:  23 MARCH 1995
      CLASSIFICATION:
    ATTORNEY/AGENT INFORMATION:
      NAME:  Perkins, Patricia Anne
      REGISTRATION NUMBER:  34,695
      REFERENCE/DOCKET NUMBER:  2617-B
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (206)587-0430
      TELEFAX:  (206)
    INFORMATION FOR SEQ ID NO:  2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 864 amino acids
      TYPE:  amino acid
      TOPOLOGY:  linear
    MOLECULE TYPE:  protein
US-09-022-696-2

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  Best Local Similarity  71.4%;  Pred. No. 3.8e-123;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

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; Patent No. 6083906
  GENERAL INFORMATION:
    APPLICANT:  Troutt, Anthony
    TITLE OF INVENTION:  Method of Regulating Nitric Oxide Production
    NUMBER OF SEQUENCES:  4
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Immunex Corporation
      STREET:  51 University Street
      CITY:  Seattle
      STATE:  WA
      COUNTRY:  USA
      ZIP:  98101
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
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      FILING DATE:
      CLASSIFICATION:  530
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  USSN 60/052,525
      FILING DATE:  27 NOVEMBER 1996
      CLASSIFICATION:  530
    ATTORNEY/AGENT INFORMATION:
      NAME:  Perkins, Patricia Anne
      REGISTRATION NUMBER:  34,693
      REFERENCE/DOCKET NUMBER:  2623-A
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (206)587-0430
      TELEFAX:  (206)
    INFORMATION FOR SEQ ID NO:  2:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  864 amino acids
      TYPE:  amino acid
      TOPOLOGY:  linear
    MOLECULE TYPE:  protein
US-08-978-773-2

  Query Match           71.1%;  Score 1254;  DB 3;  Length 864;
  Best Local Similarity  71.4%;  Pred. No. 3.8e-123;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
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; Sequence 2, Application US/09022253
; Patent No. 6096305
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6096305el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
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;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694
;      FILING DATE:  21-MARCH-1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-253-2


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  Best Local Similarity   71.4%;  Pred. No. 3.8e-123;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

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Db     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

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;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6100235el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
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;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-260-2


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  Best Local Similarity   71.4%;  Pred. No. 3.8e-123;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;
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Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
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;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6191104el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
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;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-09-022-259-2

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Query Match          71.1%;  Score 1254;  DB 4;  Length 864;
Best Local Similarity  71.4%;  Pred. No. 3.8e-123;
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Tue Jul 17 11:27:35 2001

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GenCore version 4.5
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561.333 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 412676

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1764	100.0	866	21	AAY97181	Human interleukin-
7	1764	100.0	866	21	AAB03807	Human IL-17R (hCTL
8	1764	100.0	866	22	AAB62066	Human Interleukin-
9	1764	100.0	866	22	AAY72754	Soluble IL-17R/Fla
10	1254	71.1	330	21	AAY97255	Soluble IL-17R/Fla
11	1254	71.1	330	21	AAY97258	Murine interleukin
12	1254	71.1	864	17	AAW04184	Mouse interleukin-
13	1254	71.1	864	19	AAW61271	Murine IL-17R prot
14	1254	71.1	864	20	AAW92408	Murine IL-17R prot
15	1254	71.1	864	21	AAY99935	Murine interleukin
16	1254	71.1	864	21	AAY97130	Murine interleukin
17	1254	71.1	864	21	AAY97180	Murine interleukin
18	1254	71.1	864	21	AAB03806	Murine IL-17R poly
19	1254	71.1	864	22	AAB62060	Murine Interleukin
20	1254	71.1	864	22	AAY72748	A human interleuki
21	286	16.2	426	21	AAB18750	Interleukin 17-lik
22	286	16.2	426	21	AAY70591	Human interleukin
23	286	16.2	426	21	AAY49946	A human interleuki
24	286	16.2	433	21	AAB18754	Interleukin 17-lik
25	286	16.2	433	21	AAY70595	Human PRO5801. Ho
26	286	16.2	502	22	AAB87604	Human secreted pro
27	199	11.3	385	21	AAB25795	Human secreted pro
28	199	11.3	385	22	AAB75381	Human interleukin-
29	178	10.1	34	20	AAY39426	Rat SH2 binding pr
30	90	5.1	509	19	AAW40480	Arabidopsis thalia
31	89.5	5.1	185	21	AAG58610	Tobacco mosaic vir
32	88.5	5.0	1144	17	AAR88122	Tobacco mosaic vir
33	88.5	5.0	1144	17	AAR88123	Amino acid sequenc
34	88	5.0	1210	21	AAB19259	Human EGF receptor
35	88	5.0	1210	21	AAY50616	Arabidopsis thalia
36	87.5	5.0	234	21	AAG61560	Human lysosomal me
37	87.5	5.0	410	16	AAR69555	Mouse Ret ligand R
38	85.5	4.8	397	19	AAW37461	Amino acid sequenc
39	85.5	4.8	397	21	AAY84591	Murine GFRalpha3.
40	85.5	4.8	397	21	AAY15174	Amino acid sequenc
41	84	4.8	398	21	AAY69287	Novel protein kina
42	83	4.7	862	22	AAB65669	Human IFN-gamma ac
43	81.5	4.6	337	16	AAR71035	Human lysosomal me
44	81.5	4.6	416	16	AAR69554	Human lysosomal me
45	81.5	4.6	416	21	AAY52550	

ALIGNMENTS

RESULT 1
AAW04185
ID AAW04185 standard; Protein; 866 AA.
XX
AC AAW04185;
XX
DT 05-DEC-1996 (first entry)
XX
DE Human interleukin-17 receptor.
XX
KW Interleukin-17 receptor; IL-17R; autoimmune disease; allergy;
KW asthma; graft rejection; inflammation; cytokine; therapy.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..27
FT		/label= Sig_peptide
FT	Domain	28..320
FT		/label= Extracellular_domain
FT	Domain	321..341
FT		/label= Transmembrane_domain
FT	Domain	342..866
FT		/label= Cytoplasmic_tail

XX
PN WO9629408-A1.
XX
PD 26-SEP-1996.
XX
PF 21-MAR-1996; 96WO-US04018.
XX
PR 07-AUG-1995; 95US-0538765.
PR 23-MAR-1995; 95US-0410535.
XX

```
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 1996-443184/44.
DR   N-PSDB; AAT33801.
XX
PT   DNA encoding interleukin-17 receptor - useful for regulating immune
PT   and inflammatory responses, or to suppress graft rejection
XX
PS   Claim 1; Page 41-44; 52pp; English.
XX
CC   The human interleukin-17 receptor (IL-17R) (AAW04184) is a type I
CC   transmembrane protein.  Its amino acid sequence was deduced from
CC   a cDNA clone (AAT33801) isolated from a human peripheral blood
CC   lymphocyte library.  Soluble, recombinant forms of the receptor
CC   (partic. amino acids 1-320) can be prepd. in transformed host cells
CC   and used to regulate immune and inflammatory responses, in methods
CC   for suppressing rejection of grafted organs or tissue, and in
CC   assays of IL-17 and IL-17R.
XX
SQ   Sequence   866 AA;


  Query Match             100.0%;  Score 1764;  DB 17;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-169;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
           ||||||||||||||||||||
Db     301 vscpempdtpepipdymplw 320


RESULT   2
AAW61272
ID   AAW61272 standard; Protein; 866 AA.
XX
AC   AAW61272;
XX
DT   12-OCT-1998  (first entry)
XX
DE   Human interleukin-17 receptor.
XX
KW   Interleukin-17 receptor; IL-17 receptor; human; nitric oxide;
KW   cartilage; osteoarthritis; autoimmune disease; inflammation;
KW   therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Sig_peptide
FT   Protein         28..866
FT                   /label= Mat_protein
FT   Protein         1..320
FT                   /label= Soluble_IL-17R
FT                   /note= "Claim 2(b)"
FT   Domain          28..320
FT                   /label= Extracellular
FT   Domain          321..341
FT                   /label= Transmembrane
FT   Domain          342..866
FT                   /label= Extracellular
XX
PN   WO9823284-A1.
XX
PD   04-JUN-1998.
XX
PF   21-NOV-1997;   97WO-US21451.
XX
PR   27-NOV-1996;   96US-0052525.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Troutt AB;
XX
DR   WPI; 1998-322457/28.
DR   N-PSDB; AAV27592.
XX
PT   Reducing nitric oxide production by cartilage associated cells - by
PT   contacting cells with soluble interleukin-17 receptor, useful to
PT   treat osteoarthritis and autoimmune and inflammatory diseases
XX
PS   Claim 2(b); Page 27-31; 41pp; English.
XX
CC   This polypeptide comprises human full-length interleukin-17
CC   receptor (IL-17R).  A claimed method for reducing the amount of
CC   nitric oxide produced by a cartilage associated cell comprises
CC   contacting the cell with a soluble IL-17R, especially claimed
CC   soluble human or mouse (see AAW61271) IL-17R comprising the signal
CC   peptide and extracellular domains of the respective full-length
CC   receptors.  Recombinant soluble IL-17R polypeptides can be obtained
CC   using prokaryotic or eukaryotic (for glycosylated products)
CC   expression systems.  A cDNA sequence coding for full-length human
CC   IL-17R is provided (see AAV27592).  IL-17 is known to stimulate
CC   nitric oxide production from cartilage-associated cells in
CC   individuals with osteoarthritis.  Inhibitors of nitric oxide
CC   production, such as soluble IL-17R, may therefore be useful to
CC   ameliorate the effects of nitric oxide in osteoarthritis as well as
CC   in other disease conditions in which nitric oxide plays a role,
CC   e.g. autoimmune and inflammatory diseases.
XX
SQ   Sequence   866 AA;


  Query Match             100.0%;  Score 1764;  DB 19;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-169;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy    301 VSCPEMPDTPEPIPDYMPLW 320
          ||||||||||||||||||||
Db    301 vscpempdtpepipdymplw 320


RESULT   3
AAW92409
ID   AAW92409 standard; Protein; 866 AA.
XX
AC   AAW92409;
XX
DT   21-APR-1999  (first entry)
XX
DE   Human IL-17R protein.
XX
KW   IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor;
KW   T cell proliferation; T cell activation; organ; graft; rejection;
KW   autoimmune disease; allergy; asthma; treatment; inflammatory disease;
KW   B cell proliferation; immunoglobulin secretion; immunogen.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..27
FT                    /label= signal_peptide
FT   Protein          28..866
FT                    /label= IL-17R
FT
XX
PN   US5869286-A.
XX
PD   09-FEB-1999.
XX
PF   21-MAR-1996;    96US-0620694.
XX
PR   21-MAR-1996;    96US-0620694.
PR   23-MAR-1995;    95US-0410535.
PR   07-AUG-1995;    95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 1999-152766/13.
DR   N-PSDB; AAX01922.
XX
PT   Isolated interleukin-17 receptor DNA - used to develop products for
PT   treating e.g. organ or graft rejection, autoimmune disease, allergy,
PT   asthma or inflammatory disease
XX
PS   Disclosure; Column 43-48; 25pp; English.
XX
CC   This sequence represents a human interleukin-17 receptor (IL-17R).
CC   IL-17R polypeptides have immunoregulatory activity. They can be used for
CC   inhibiting T cell proliferation, or for inhibiting T cell activation. In
CC   particular they can be used for preventing or treating organ or graft
CC   rejection, autoimmune disease, allergy or asthma. They can also be used
CC   for the prevention or treatment of inflammatory disease in which
CC   activated T cells play a role or for inhibiting B cell proliferation
CC   or immunoglobulin secretion. The IL-17 polypeptides can also be used
CC   as immunogens, reagents in in vitro assays, or as binding agents for
CC   affinity purification procedures.
XX
SQ   Sequence   866 AA;


  Query Match           100.0%;  Score 1764;  DB 20;  Length 866;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-169;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db.      1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
          ||||||||||||||||||||
Db     301 vscpempdtpepipdymplw 320


RESULT   4
AAY99941
ID   AAY99941 standard; Protein; 866 AA.
XX
AC   AAY99941;
XX
DT   10-JAN-2001  (first entry)
XX
DE   Human IL-17R protein.
XX
KW   IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
KW   murine; antibody; immune suppression.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..27
FT                    /label= Signal_peptide
FT   Domain           28..320
FT                    /label= Extracellular_domain
FT   Domain           321..341
FT                    /label= Transmembrane_domain
FT   Domain           342..866
FT                    /label= Cytoplasmic_domain
FT   Protein          32..866
FT                    /label= IL-17R
FT
XX
PN   US6072037-A.
XX
PD   06-JUN-2000.
XX
PF   12-FEB-1998;    98US-0022696.
XX
PR   21-MAR-1996;    96US-0620694.
PR   23-MAR-1995;    95US-0538765.
PR   07-AUG-1995;    95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-411206/35.
DR   N-PSDB; AAA61240.
XX
PT   Antibodies immunoreactive with interleukin-17 receptor protein useful
PT   in interfering with receptor binding to CTLA-8, as components of
PT   diagnostic or research assays or in affinity purification of the
PT   receptor -
XX
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PS   Claim 1; Column 43-48; 25pp; English.
XX
CC   The present invention relates to a novel receptor that binds Interleukin
CC   17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC   HVS13. The receptor is a type I transmembrane protein which is referred
CC   to as IL-17R. Murine thymona EL4 cells were found to express a
CC   receptor for IL-17. An EL4 mammalian expression library was screened
CC   and a cDNA encoding the receptor was identified. The murine IL-17R cDNA
CC   and protein are described in AAA61238 and AAY99935. The cDNA was used to
CC   isolate DNA encoding human IL-17R by cross species hybridisation. The
CC   present sequence is the human IL-7R protein. Soluble forms of the
CC   receptor may be used to regulate immune responses, for example to
CC   suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC   amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be
CC   useful as components of diagnostic or research assays. Such antibodies
CC   may also be used in affinity purification of the receptor.
XX
SQ   Sequence   866 AA;


  Query Match                 100.0%;  Score 1764;  DB 21;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-169;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
             ||||||||||||||||||||
Db     301 vscpempdtpepipdymplw 320


RESULT   5
AAY97131
ID   AAY97131 standard; Protein; 866 AA.
XX
AC   AAY97131;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Human interleukin-17 receptor.
XX
KW   IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW   HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW   anti-asthmatic.
XX
OS   Homo sapiens.
XX
FH   Key
FT   Peptide          Location/Qualifiers
FT                    1..27
FT                    /label= Signal_peptide
FT   Protein          28..866
FT                    /label= Mature_protein
FT                    1..320
FT   Domain           /label= Soluble_IL-17_receptor
                      28..320
FT
FT   Domain           /label= Extracellular_domain
FT                    321..341
FT   Domain           /label= Transmembrane_domain
FT                    342..866
XX                    /label= Cytoplasmic_tail
PN   US6100235-A.
XX
PD   08-AUG-2000.
XX
PF   11-FEB-1998;   98US-0022260.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-548298/50.
DR   N-PSDB; AAA51988.
XX
PT   Regulating, treating or preventing immune or inflammatory response in a
PT   mammal, especially organ or graft rejection, allergy or asthma,
PT   comprises administering interleukin-17 receptors
XX
PS   Claim 1; Column 43-48; 26pp; English.
XX
CC   A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC   cDNA library from T cell thymoma EL4 cells, which were identified as
CC   binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC   region and soluble IL-17 (CTLA-8) protein or a homologous
CC   Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an
CC   immune or inflammatory response in a mammal comprises administering
CC   soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the
CC   murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the
CC   extracellular domain that bind IL-17. The method is useful for regulating
CC   an immunoresponse, for treating or preventing diseases like allergy,
CC   asthma and autoimmune diseases, and for suppressing rejection of grafted
CC   organs or tissues in the recipient.
XX
SQ   Sequence   866 AA;


  Query Match                 100.0%;  Score 1764;  DB 21;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-169;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
             ||||||||||||||||||||
Db     301 vscpempdtpepipdymplw 320
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RESULT   6
AAY97181
ID   AAY97181 standard; Protein; 866 AA.
XX
AC   AAY97181;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Human interleukin-17 receptor.
XX
KW   IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW   HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW   anti-asthmatic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Signal_peptide
FT   Protein         28..866
FT                   /label= Mature_protein
FT   Protein         1..320
FT                   /label= Soluble_IL-17_receptor
FT   Domain          28..320
FT                   /label= Extracellular_domain
FT   Domain          321..341
FT                   /label= Transmembrane_domain
FT   Domain          342..866
FT                   /label= Cytoplasmic_tail
XX
PN   US6096305-A.
XX
PD   01-AUG-2000.
XX
PF   11-FEB-1998;    98US-0022253.
XX
PR   21-MAR-1996;    96US-0620694.
PR   23-MAR-1995;    95US-0410535.
PR   07-AUG-1995;    95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-523862/47.
DR   N-PSDB; AAA52146.
XX
PT   Suppressing rejection of a grafted syngeneic or allogeneic organ or
PT   tissue in a graft recipient for organ transplantation involves
PT   transfecting the organ or tissue with DNA encoding soluble
PT   interleukin-17 receptor
XX
PS   Claim 1; Column 43-48; 27pp; English.
XX
CC   A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC   cDNA library from T cell thymoma EL4 cells, which were identified as
CC   binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC   region and soluble IL-17 (CTLA-8) protein or a homologous
CC   Herpesvirus saimiri (HSV) protein, designated HSV13. Suppressing
CC   rejection of a grafted syngeneic or allogeneic organ or tissue in a graft
CC   recipient involves transfecting the organ or tissue to be transplanted
CC   with DNA encoding soluble IL-17R, so that expression of IL-17R by the
CC   engrafted organ or tissue results in suppression of rejection. Soluble
CC   IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues
CC   1-320 of the human IL-17R, and fragments of the extracellular domain
CC   that bind IL-17. The method is useful for regulating an immunoresponse,
CC   for suppressing rejection of grafted organs or tissues in the recipient
CC   and for treating or preventing diseases like allergy, asthma and
CC   autoimmune diseases.
XX
SQ   Sequence   866 AA;
```

```
 Query Match           100.0%;  Score 1764;  DB 21;  Length 866;
 Best Local Similarity  100.0%;  Pred. No. 1.7e-169;
 Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
           ||||||||||||||||||||
Db     301 vscpempdtpepipdymplw 320
```

```
RESULT   7
AAB03807
ID   AAB03807 standard; Protein; 866 AA.
XX
AC   AAB03807;
XX
DT   13-OCT-2000  (first entry)
XX
DE   Human interleukin-17 (IL-17) receptor protein sequence.
XX
KW   Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; antiallergic;
KW   immunosuppressive; organ rejection; graft rejection; autoimmune disease;
KW   allergy; asthma; human.
XX
OS   Homo sapiens.
XX
PN   US6072033-A.
XX
PD   06-JUN-2000.
XX
PF   11-FEB-1998;    98US-0022255.
XX
PR   21-MAR-1996;    96US-0620694.
PR   23-MAR-1995;    95US-0410535.
PR   07-AUG-1995;    95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-411205/35.
DR   N-PSDB; AAA59871.
XX
PT   Interleukin-17 receptor protein useful for regulating immune functions
PT   and for preventing or treating organ or graft rejection, autoimmune
PT   disease, allergy or asthma in human
XX
PS   Claim 1; Column 43-48; 26pp; English.
XX
CC   This invention relates to an isolated and purified interleukin-17
CC   receptor (IL-17R). A soluble IL-17 protein (CTLA8) and a herpesvirus
CC   siamiri (HVS13) open reading frame (homologous to CTLA8) were expressed
CC   as fusion proteins comprising an immunoglobulin Fc region, and used to
```

```
CC   screen for the expression of the IL-17R. The screening identified the
CC   novel receptor of the invention. IL-17R is a type I transmembrane
CC   protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic
CC   and antiallergic activities, and is an inhibitor of T cell proliferation
CC   and activation. IL-17R can be used to regulate immune functions, and is
CC   useful for preventing or treating organ or graft rejection, autoimmune
CC   disease, allergy or asthma. The present sequence represents the human
CC   interleukin-17 receptor amino acid sequence identified in the invention.
XX
SQ   Sequence   866 AA;


  Query Match             100.0%;  Score 1764;  DB 21;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-169;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
          ||||||||||||||||||||
Db     301 vscpempdtpepipdymplw 320


RESULT   8
AAB62066
ID   AAB62066 standard; Protein; 866 AA.
XX
AC   AAB62066;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Human IL-17R (hCTLA-8 receptor) polypeptide.
XX
KW   CTLA-8; interleukin-17; IL-17; IL-17 receptor; IL-17R; human;
KW   immunosuppressive; antiallergic; antiasthmatic; antiinflammatory.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /note= "signal peptide"
FT   Protein         28..866
FT                   /note= "mature protein"
FT   Domain          28..320
FT                   /note= "extracellular domain"
FT   Domain          321..341
FT                   /note= "transmembrane domain"
FT   Domain          342..866
FT                   /note= "cytoplasmic domain"
XX
PN   US6197525-B1.
XX
PD   06-MAR-2001.
XX
PF   11-FEB-1998;   98US-0022257.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Yao Z,  Spriggs MK,  Fanslow WC;
XX
DR   WPI; 2001-234480/24.
DR   N-PSDB; AAF57188.
XX
PT   New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors
PT   and (antagonists or mimetics of) the interaction between IL-17 and
PT   IL-17 receptor, useful for treating autoimmune diseases -
XX
PS   Claim 1; Columns 37-44; 26pp; English.
XX
CC   The invention is directed towards assays for detection of interleukin-17
CC   (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the
CC   interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R
CC   protein and a detecting reagent. The method is useful for inhibiting
CC   binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also
CC   useful for preventing or treating organ or graft rejection, autoimmune
CC   diseases, allergy, asthma and inflammatory diseases in which activated
CC   T-cells play an important role. The present sequence represents a
CC   human IL-17R (hCTLA-8 receptor) polypeptide.
XX
SQ   Sequence   866 AA;


  Query Match             100.0%;  Score 1764;  DB 22;  Length 866;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-169;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
          ||||||||||||||||||||
Db     301 vscpempdtpepipdymplw 320


RESULT   9
AAY72754
ID   AAY72754 standard; Protein; 866 AA.
XX
AC   AAY72754;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Human Interleukin-17 receptor (IL-17R) or CTLA-8 receptor.
XX
KW   Human; Interleukin-17 receptor; IL-17R; immunosuppressive; antiallergic;
KW   antiasthmatic; antiinflammatory; graft rejection; autoimmune disease;
KW   inflammatory disease; allergy; CTLA-8; immunogen; asthma.
```

```
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  Peptide         1..27
FT                  /label= Signal_peptide
FT
FT  Protein         28..866
FT                  /label= Mature_human_IL-17_receptor
FT
FT  Domain          28..320
FT                  /label= Extracellular_domain
FT
FT  Domain          321..341
FT                  /label= Transmembrane_domain
FT
FT  Domain          342..866
FT                  /label= Cytoplasmic_tail
FT
XX
PN  US6191104-B1.
XX
PD  20-FEB-2001.
XX
PF  11-FEB-1998;    98US-0022259.
XX
PR  21-MAR-1996;    96US-0620694.
PR  23-MAR-1995;    95US-0410535.
PR  07-AUG-1995;    95US-0538765.
XX
PA  (IMMV ) IMMUNEX CORP.
XX
PI  Spriggs MK,  Fanslow WC;
XX
DR  WPI; 2001-217901/22.
DR  N-PSDB; AAD02815.
XX
PT  Suppressing rejection of grafted organ or tissue in graft recipient,
PT  involves administering to recipient a composition comprising
PT  interleukin 17 receptor protein -
XX
PS  Claim 1; Column 43-48; 26pp; English.
XX
CC  The present sequence is human Interleukin-17 receptor (IL-17R) or
CC  CTLA-8 receptor. Human IL-17R is isolated from a human peripheral
CC  blood lymphocyte library by cross-species hybridisation.
CC  The invention relates to Interleukin-17 receptors (IL-17R),
CC  Interleukin-17 and their corresponding nucleic acid molecules. IL-17R is
CC  a Type I transmembrane protein which is used for regulating the immune
CC  response. The invention is useful for suppressing rejection of a grafted
CC  organ or tissue in a graft recipient. Soluble IL-17 (CTLA-8) receptors
CC  are useful for preventing or treating organ or graft rejection,
CC  autoimmune disease, allergy, asthma, and inflammatory disease in which
CC  activated T-cells play a role. Soluble IL-17 fusion proteins are used to
CC  screen cells for the expression of IL-17 receptor. Derivatives of IL-17R
CC  are also used as immunogens, reagents in in vitro assays, or as binding
CC  agents for affinity purification procedures.
XX
SQ  Sequence   866 AA;

  Query Match           100.0%;  Score 1764;  DB 22;  Length 866;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-169;
  Matches  320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VSCPEMPDTPEPIPDYMPLW 320
           ||||||||||||||||||||
Db     301 vscpempdtpepipdymplw 320


RESULT  10
AAY97255
ID  AAY97255 standard; peptide; 330 AA.
XX
AC  AAY97255;
XX
DT  04-DEC-2000  (first entry)
XX
DE  Soluble IL-17R/Flag fusion protein.
XX
KW  IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW  HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW  anti-asthmatic; Flag epitope; fusion protein.
XX
OS  Mus sp.
XX
FH  Key             Location/Qualifiers
FT  Protein         1..322
FT                  /label= Soluble_IL-17_receptor
FT
FT  Peptide         1..31
FT                  /label= Signal_peptide
FT
FT  Protein         32..322
FT                  /label= IL-17_receptor_extracellular_domain
FT
FT  Peptide         323..330
FT                  /label= Flag_epitope
FT
XX
PN  US6096305-A.
XX
PD  01-AUG-2000.
XX
PF  11-FEB-1998;    98US-0022253.
XX
PR  21-MAR-1996;    96US-0620694.
PR  23-MAR-1995;    95US-0410535.
PR  07-AUG-1995;    95US-0538765.
XX
PA  (IMMV ) IMMUNEX CORP.
XX
PI  Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR  WPI; 2000-523862/47.
XX
PT  Suppressing rejection of a grafted syngeneic or allogeneic organ or
PT  tissue in a graft recipient for organ transplantation involves
PT  transfecting the organ or tissue with DNA encoding soluble
PT  interleukin-17R receptor
XX
PS  Example 3; Column -; 27pp; English.
XX
CC  A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC  cDNA library from T cell thymoma EL4 cells, which were identified as
CC  binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC  region and soluble IL-17 (CTLA-8) protein or a homologous
CC  Herpesvirus saimiri (HSV) protein, designated HSV13. Suppressing
CC  rejection of a grafted syngeneic or allogeneic organ or tissue in a
CC  graft recipient involves transfecting the organ or tissue to be
CC  transplanted with DNA encoding soluble IL-17R, so that expression of
CC  IL-17R by the engrafted organ or tissue results in suppression of
CC  rejection. Soluble IL-17R fragments comprise residues 1-322 of the murine
CC  IL-17R, residues 1-320 of the human IL-17R, and fragments of the
CC  extracellular domain that bind IL-17. The method is useful for regulating
```

```
CC   an immunoresponse, for suppressing rejection of grafted organs or tissues
CC   in the recipient and for treating or preventing diseases like allergy,
CC   asthma and autoimmune diseases.
CC   Note: This sequence does not appear in the specification. It was created
CC   from the full length murine IL-17R (see AAY97180) and the flag peptide
CC   (see AAY97183)
XX
SQ   Sequence   330 AA;


  Query Match             71.1%;  Score 1254;  DB 21;  Length 330;
  Best Local Similarity   71.4%;  Pred. No. 1.7e-118;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           |||||:|||||||::| |  |   : || |:| || |:|||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||||:||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||| ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||: :  | ||| |||||||:||| ||      || | ||:||||||||||||||: |
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VSCPEMPDT--PEPIPDYMPLW 320
           | || : :|  |:|: ||:|||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT  11
AAY97258
ID   AAY97258 standard; peptide; 330 AA.
XX
AC   AAY97258;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Soluble IL-17R/Flag fusion protein.
XX
KW   IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW   HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW   anti-asthmatic; Flag epitope; fusion protein.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..322
FT                   /label= Soluble_IL-17_receptor
FT   Peptide         1..31
FT                   /label= Signal_peptide
FT   Protein         32..322
FT                   /label= IL-17_receptor_extracellular_domain
FT   Peptide         323..330
FT                   /label= Flag_epitope
XX
PN   US6100235-A.
XX
PD   08-AUG-2000.
XX
PF   11-FEB-1998;   98US-0022260.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-548298/50.
XX
PT   Regulating, treating or preventing immune or inflammatory response in a
PT   mammal, especially organ or graft rejection, allergy or asthma,
PT   comprises administering interleukin-17 receptors
XX
PS   Example 3; Column -; 27pp; English.
XX
CC   A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC   cDNA library from T cell thymoma EL4 cells, which were identified as
CC   binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC   region and soluble IL-17 (CTLA-8) protein or a homologous
CC   Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an
CC   immune or inflammatory response in a mammal comprises administering
CC   soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the
CC   murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the
CC   extracellular domain that bind IL-17. The method is useful for
CC   regulating an immunoresponse, for treating or preventing diseases like
CC   allergy, asthma and autoimmune diseases, and for suppressing rejection of
CC   grafted organs or tissues in the recipient.
CC   Note: This sequence does not appear in the specification. It was created
CC   from the full length murine IL-17R (see AAY97130) and the flag peptide
CC   (see AAY97132)
XX
SQ   Sequence   330 AA;


  Query Match             71.1%;  Score 1254;  DB 21;  Length 330;
  Best Local Similarity   71.4%;  Pred. No. 1.7e-118;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           |||||:|||||||::| |  |   : || |:| || |:|||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||||:||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||| ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||: :  | ||| |||||||:||| ||      || | ||:||||||||||||||: |
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VSCPEMPDT--PEPIPDYMPLW 320
           | || : :|  |:|: ||:|||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT  12
AAW04184
ID   AAW04184 standard; Protein; 864 AA.
XX
AC   AAW04184;
XX
DT   05-DEC-1996  (first entry)
XX
DE   Murine interleukin-17 receptor.
XX
KW   Interleukin-17 receptor; IL-17R; autoimmune disease; allergy;
```

```
KW   asthma; graft rejection; inflammation; cytokine; therapy.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= Sig_peptide
FT
FT   Domain          32..322
FT                   /label= Extracellular_domain
FT
FT   Domain          323..343
FT                   /label= Transmembrane_domain
FT
FT   Domain          344..864
FT                   /label= Cytoplasmic_tail
FT
XX
PN   WO9629408-A1.
XX
PD   26-SEP-1996.
XX
PF   21-MAR-1996;    96WO-US04018.
XX
PR   07-AUG-1995;    95US-0538765.
PR   23-MAR-1995;    95US-0410535.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 1996-443184/44.
DR   N-PSDB; AAT33800.
XX
PT   DNA encoding interleukin-17 receptor - useful for regulating immune
PT   and inflammatory responses, or to suppress graft rejection
XX
PS   Claim 1; Page 29-32; 52pp; English.
XX
CC   The murine interleukin-17 receptor (IL-17R) (AAW04184) is a type I
CC   transmembrane protein that binds IL-17 (CTLA-8, see also AAW02386)
CC   and HVS13 (AAW02387), a viral homologue of IL-17.  Its amino acid
CC   sequence was deduced from a cDNA clone (AAT33800) isolated from murine
CC   thymoma EL4 cells.  Soluble, recombinant forms of the receptor
CC   (partic. amino acids 1-322) can be prepd. in transformed host cells
CC   and used to regulate immune and inflammatory responses, in methods
CC   for suppressing rejection of grafted organs or tissue, and in
CC   assays of IL-17 and IL-17R.
XX
SQ   Sequence   864 AA;

  Query Match          71.1%;  Score 1254;  DB 17;  Length 864;
  Best Local Similarity  71.4%;  Pred. No. 6.7e-118;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
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Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           |||||:|||||||:: | |  : || |:| || |:||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||:||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||| ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           |||||| :  | ||| |||||||:||| ||     || | ||:|||||||||||||: |
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VSCPEMPDT--PEPIPDYMPLW 320
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```
           | || : :|  |:|: ||:|||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT  13
AAW61271
ID   AAW61271 standard; Protein; 864 AA.
XX
AC   AAW61271;
XX
DT   12-OCT-1998  (first entry)
XX
DE   Mouse interleukin-17 receptor.
XX
KW   Interleukin-17 receptor; IL-17 receptor; mouse; nitric oxide;
KW   cartilage; osteoarthritis; autoimmune disease; inflammation;
KW   therapy.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= Sig_peptide
FT
FT   Protein         32..864
FT                   /label= Mat_protein
FT
FT   Protein         1..322
FT                   /label= Soluble_IL-17R
FT                   /note= "Claim 2(a)"
FT
FT   Domain          32..322
FT                   /label= Extracellular
FT
FT   Domain          323..343
FT                   /label= Transmembrane
FT
FT   Domain          344..864
FT                   /label= Extracellular
FT
XX
PN   WO9823284-A1.
XX
PD   04-JUN-1998.
XX
PF   21-NOV-1997;    97WO-US21451.
XX
PR   27-NOV-1996;    96US-0052525.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Troutt AB;
XX
DR   WPI; 1998-322457/28.
DR   N-PSDB; AAV27591.
XX
PT   Reducing nitric oxide production by cartilage associated cells - by
PT   contacting cells with soluble interleukin-17 receptor, useful to
PT   treat osteoarthritis and autoimmune and inflammatory diseases
XX
PS   Claim 2(a); Page 20-23; 41pp; English.
XX
CC   This polypeptide comprises mouse full-length interleukin-17
CC   receptor (IL-17R).  A claimed method for reducing the amount of
CC   nitric oxide produced by a cartilage associated cell comprises
CC   contacting the cell with a soluble IL-17R, especially claimed
CC   soluble murine or human (see AAW61272) IL-17R comprising the signal
CC   peptide and extracellular domains of the respective full-length
CC   receptors.  Recombinant soluble IL-17R polypeptides can be obtained
CC   using prokaryotic or eukaryotic (for glycosylated products)
CC   expression systems.  A cDNA sequence (see AAV27591) coding for
CC   full-length murine IL-17R is provided.  IL-17 is known to stimulate
CC   nitric oxide production from cartilage-associated cells in
CC   individuals with osteoarthritis.  Inhibitors of nitric oxide
CC   production, such as soluble IL-17R, may therefore be useful to
CC   ameliorate the effects of nitric oxide in osteoarthritis as well
CC   as in other disease conditions in which nitric oxide plays a role,
CC   e.g. autoimmune and inflammatory diseases.
XX
```

SQ Sequence 864 AA;

Query Match 71.1%; Score 1254; DB 19; Length 864;
Best Local Similarity 71.4%; Pred. No. 6.7e-118;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

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           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           |||||:||||||||:: | |  : || |:| || |:|||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||:||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||| ::||:|| |:|||||||||||||:   ||| |||||||| ||:|| ||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||: :  | ||| ||||||:||| ||     || | ||:||||||||||||||: |
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VSCPEMPDT--PEPIPDYMPLW 320
           | || : :|  |:|: ||:|||
Db     301 vpcpvisnttvpkpvadyiplw 322
```

RESULT 14
AAW92408
ID AAW92408 standard; Protein; 864 AA.
XX
AC AAW92408;
XX
DT 21-APR-1999 (first entry)
XX
DE Murine IL-17R protein.
XX
KW IL-17R; murine; interleukin-17 receptor; immunoregulator; inhibitor;
KW T cell proliferation; T cell activation; organ; graft; rejection;
KW autoimmune disease; allergy; asthma; treatment; inflammatory disease;
KW B cell proliferation; immunoglobulin secretion; immunogen.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= signal_peptide
FT Protein 32..864
XX
PN US5869286-A.
XX
PD 09-FEB-1999.
XX
PF 21-MAR-1996; 96US-0620694.
XX
PR 21-MAR-1996; 96US-0620694.
PR 23-MAR-1995; 95US-0410535.
PR 07-AUG-1995; 95US-0538765.
XX
PA . (IMMV) IMMUNEX CORP.
XX
PI Fanslow WC, Spriggs MK, Yao Z;
XX
DR WPI; 1999-152766/13.
DR N-PSDB; AAX01921.
XX
PT Isolated interleukin-17 receptor DNA - used to develop products for
PT treating e.g. organ or graft rejection, autoimmune disease, allergy,
PT asthma or inflammatory disease
XX
PS Disclosure; Column 25-30; 25pp; English.
XX
CC This sequence represents a murine interleukin-17 receptor (IL-17R).
CC IL-17R polypeptides have immunoregulatory activity. They can be used for
CC inhibiting T cell proliferation, or for inhibiting T cell activation. In
CC particular they can be used for preventing or treating organ or graft
CC rejection, autoimmune disease, allergy or asthma. They can also be used
CC for the prevention or treatment of inflammatory disease in which
CC activated T cells play a role or for inhibiting B cell proliferation
CC or immunoglobulin secretion. The IL-17 polypeptides can also be used
CC as immunogens, reagents in in vitro assays, or as binding agents for
CC affinity purification procedures.
XX
SQ Sequence 864 AA;

Query Match 71.1%; Score 1254; DB 20; Length 864;
Best Local Similarity 71.4%; Pred. No. 6.7e-118;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

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           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           |||||:||||||||:: | |  : || |:| || |:|||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||:||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
           ||||| ::||:|| |:|||||||||||||:   ||| |||||||| ||:|| ||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||: :  | ||| ||||||:||| ||     || | ||:||||||||||||||: |
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VSCPEMPDT--PEPIPDYMPLW 320
           | || : :|  |:|: ||:|||
Db     301 vpcpvisnttvpkpvadyiplw 322
```

RESULT 15
AAY99935
ID AAY99935 standard; Protein; 864 AA.
XX
AC AAY99935;
XX
DT 10-JAN-2001 (first entry)
XX
DE Murine IL-17R protein.
XX
KW IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
KW murine; antibody; immune suppression.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= Signal_peptide
FT Domain 32..322
FT /label= Extracellular_domain
FT Domain 323..353
FT /label= Transmembrane_domain
FT Domain 354..864
FT /label= Cytoplasmic_domain
FT Protein 32..864
FT /label= IL-17R

XX
PN US6072037-A.
XX
PD 06-JUN-2000.
XX
PF 12-FEB-1998; 98US-0022696.
XX
PR 21-MAR-1996; 96US-0620694.
PR 23-MAR-1995; 95US-0410535.
PR 07-AUG-1995; 95US-0538765.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Fanslow WC, Spriggs MK, Yao Z;
XX
DR WPI; 2000-411206/35.
DR N-PSDB; AAA61238.
XX
PT Antibodies immunoreactive with interleukin-17 receptor protein useful
PT in interfering with receptor binding to CTLA-8, as components of
PT diagnostic or research assays or in affinity purification of the
PT receptor -
XX
PS Claim 1; Column 25-30; 25pp; English.
XX
CC The present invention relates to a novel receptor that binds Interleukin
CC 17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC HVS13. The receptor is a type I transmembrane protein which is referred
CC to as IL-17R. Murine thymona EL4 cells were found to express a
CC receptor for IL-17. An EL4 mammalian expression library was screened
CC and a cDNA encoding the receptor was identified. The present sequence
CC is the murine IL-7R protein. The cDNA was used to isolate DNA encoding
CC human IL-17R by cross species hybridisation. The human IL-17R cDNA and
CC protein are described in AAA61240 and AAY99941. Soluble forms of the
CC receptor may be used to regulate immune responses, for example to
CC suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be useful
CC as components of diagnostic or research assays. Such antibodies may also
CC be used in affinity purification of the receptor.
XX
SQ Sequence 864 AA;

Query Match 71.1%; Score 1254; DB 21; Length 864;
Best Local Similarity 71.4%; Pred. No. 6.7e-118;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

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Qy       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
           |||||:||||||||:: | |  : || |:| || |:|||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
           ||||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||:||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
            ||||| ::||:|| |:||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
           ||||||: :  | ||| ||||||:||| ||     || | ||:||||||||||||: |
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VSCPEMPDT--PEPIPDYMPLW 320
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Db     301 vpcpvisnttvpkpvadyiplw 322
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Search completed: July 17, 2001, 11:18:55
Job time: 194 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:18:01 ; Search time 38.21 Seconds
(without alignments)
1114.949 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCWPRVVPGPALGWLL.....CPVISNTTVPKPVADYIPLW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1766	100.0	864	11	Q60943	Q60943 mus musculu
2	1254	71.0	866	4	O43844	O43844 homo sapien
3	282.5	16.0	426	4	Q9NRL4	Q9nrl4 homo sapien
4	280.5	15.9	502	4	Q9NRM6	Q9nrm6 homo sapien
5	247.5	14.0	499	11	Q9JIP3	Q9jip3 mus musculu
6	231	13.1	288	4	Q9NRM5	Q9nrm5 homo sapien
7	140.5	8.0	218	11	Q9JIP2	Q9jip2 mus musculu
8	112.5	6.4	708	3	Q9P7H9	Q9p7h9 schizosacch
9	99.5	5.6	1506	13	P79927	P79927 xenopus lae
10	97.5	5.5	328	14	Q9IU91	Q9iu91 human immun
11	94.5	5.4	592	11	Q9JLN5	Q9jln5 mus musculu
12	92	5.2	682	10	Q9FX72	Q9fx72 arabidopsis
13	91.5	5.2	3131	3	O42926	O42926 schizosacch
14	91	5.2	333	5	O62453	O62453 caenorhabdi
15	89.5	5.1	1815	5	Q22531	Q22531 caenorhabdi
16	88	5.0	1231	5	Q17024	Q17024 anopheles g
17	88	5.0	1323	3	O13686	O13686 schizosacch
18	87.5	5.0	416	10	Q9SVG6	Q9svg6 arabidopsis
19	87.5	5.0	1188	5	O76326	O76326 drosophila
20	87	4.9	2515	5	Q9W2J8	Q9w2j8 drosophila
21	86.5	4.9	920	5	Q9VPB7	Q9vpb7 drosophila
22	86.5	4.9	947	14	Q9E964	Q9e964 ryegrass mo
23	85.5	4.8	356	2	Q9R2Z1	Q9r2z1 vibrio chol
24	85.5	4.8	562	10	Q9SSG8	Q9ssg8 arabidopsis
25	85.5	4.8	1280	5	Q9VY47	Q9vy47 drosophila
26	85	4.8	925	4	Q9UJB2	Q9ujb2 homo sapien
27	85	4.8	985	4	Q9UJB3	Q9ujb3 homo sapien
28	85	4.8	1082	13	Q9PWG9	Q9pwg9 xenopus lae
29	84.5	4.8	712	10	O80773	O80773 arabidopsis
30	84.5	4.8	969	5	Q9VLL1	Q9vll1 drosophila
31	84.5	4.8	1388	4	Q9NS87	Q9ns87 homo sapien
32	84	4.8	430	14	Q9WRE3	Q9wre3 human immun
33	84	4.8	574	4	Q9P2L8	Q9p218 homo sapien
34	83.5	4.7	304	2	Q9I5A6	Q9i5a6 pseudomonas
35	83.5	4.7	432	14	Q9Q922	Q9q922 shope fibro
36	83.5	4.7	880	5	Q9V4N0	Q9v4n0 drosophila
37	83.5	4.7	1349	11	Q9WVT0	Q9wvt0 rattus norv
38	83	4.7	431	4	Q15137	Q15137 homo sapien
39	83	4.7	868	11	Q9R094	Q9r094 mus musculu
40	83	4.7	4688	2	Q9PQ08	Q9pq08 ureaplasma
41	82.5	4.7	399	14	O92407	O92407 bombyx mori
42	82.5	4.7	565	2	Q47634	Q47634 escherichia
43	82.5	4.7	565	2	Q47635	Q47635 shigella fl
44	82.5	4.7	692	5	Q9W5Z0	Q9w5z0 drosophila
45	82.5	4.7	1030	5	Q17443	Q17443 caenorhabdi

ALIGNMENTS

RESULT 1
Q60943
ID Q60943 PRELIMINARY; PRT; 864 AA.
AC Q60943;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 17 RECEPTOR.
GN IL17R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMOMA EL4;
RX MEDLINE=96111968; PubMed=8777726;
RA Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,
RA Comeau M.R., Cohen J.I., Spriggs M.K.;
RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a
RT novel cytokine receptor.";
RL Immunity 3:811-821(1995).
DR EMBL; U31993; AAC52357.1; -.
DR MGD; MGI:107399; Il17r.
SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 100.0%; Score 1766; DB 11; Length 864;
Best Local Similarity 100.0%; Pred. No. 5.9e-163;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
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Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           ||||||||||||||||||||||
Db     301 VPCPVISNTTVPKPVADYIPLW 322


RESULT   2
O43844
ID   O43844      PRELIMINARY;      PRT;   866 AA.
AC   O43844;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   IL-17 RECEPTOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98035683; PubMed=9367539;
RA   Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,
RA   VandenBos T., Zappone J., Painter S.L., Armitage R.J.;
RT   "Molecular characterization of the human interleukin (IL)-17
RT   receptor.";
RL   Cytokine 9:794-800(1997).
DR   EMBL; U58917; AAB99730.1; -.
SQ   SEQUENCE   866 AA;  96121 MW;  88AF626A83F3FF70 CRC64;


  Query Match             71.0%;  Score 1254;  DB 4;  Length 866;
  Best Local Similarity   71.4%;  Pred. No. 3.1e-113;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           |||||:|||||||:: | |  : || |:| || |:|||||||||||||||||||||||||
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           |||||||:|:||| |:|| :||||:|||||||| |||||||||||||||||:||
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           |||||  ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||: :  | ||| ||||||:||| ||     || | ||:|||||||||||||: |
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           | || : :|  |:|: ||:|||
Db     301 VSCPEMPDT--PEPIPDYMPLW 320


RESULT   3
Q9NRL4
ID   Q9NRL4      PRELIMINARY;      PRT;   426 AA.
AC   Q9NRL4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   IL-17B RECEPTOR.
GN   IL17BR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20317118; PubMed=10749887;
RA   Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
RA   Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,
RA   Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
RA   Carrell J.A., Ebner R.;
RT   "A novel cytokine receptor-ligand pair. Identification, molecular
RT   characterization, and in vivo immunomodulatory activity.";
RL   J. Biol. Chem. 275:19167-19176(2000).
DR   EMBL; AF212365; AAF78776.1; -.
KW   Receptor.
SQ   SEQUENCE   426 AA;  47137 MW;  D5B820CCEFC12E27 CRC64;


  Query Match             16.0%;  Score 282.5;  DB 4;  Length 426;
  Best Local Similarity   28.2%;  Pred. No. 3e-19;
  Matches   89;  Conservative   50;  Mismatches  138;  Indels   39;  Gaps   11;

Qy      20 LLLLNVLAPGR-ASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNIYI 78
           |:||:: |  | | ||    |   |  |          |      |:   :| |   ::: :
Db       3 LVLLSLAALCRSAVPR---EPTVQCGSE---------TGPSPEWMLQHDLIPGDLRDLRV 50

Qy      79 NLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL-QLNTNERLCVKFQFLSMLQH 137
             :|   |:   :::| | |: |||| |:  :: |  : |     ||:  :    |
Db      51 EPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQT 110

Qy     138 HRK----RWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMKMT 193
           :    :| ||:  | |:    | :  |::|    : |    |     | | |  ||
Db     111 QTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170

Qy     194 TSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIF 253
           || :|||||||||    : : : |:||       |  |::       ||      |:|
Db     171 KKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQ-------HSTIIGFSQVF 223

Qy     254 APRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVP-CPVISNTTVP 312
           | |::   ||:|   ::          ||: |:| :| :||:||  ||  ||    | ||
Db     224 EPHQKK-QTRASVVIPVTGDSEGA--TVQLTPYFPTCGSDCIRHKGTVVLCP---QTGVP 277

Qy     313 KPV-------ADYIPL 321
           |:         ::||
Db     278 FPLDNNKSKPGGWLPL 293


RESULT   4
Q9NRM6
ID   Q9NRM6      PRELIMINARY;      PRT;   502 AA.
AC   Q9NRM6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   IL-17 RECEPTOR HOMOLOG PRECURSOR.
GN   EVI27.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20273223; PubMed=10815801;
RA   Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
RA   Shaughnessy J.D. Jr.;
RT   "Evi27 encodes a novel membrane protein with homology to the IL17
RT   receptor.";
RL   Oncogene 19:2098-2109(2000).
DR   EMBL; AF208110; AAF86051.1; -.
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KW   Signal; Receptor.
FT   SIGNAL       1     13       POTENTIAL.
FT   CHAIN        14    502      IL-17 RECEPTOR HOMOLOG.
SQ   SEQUENCE   502 AA;  55918 MW;  9C84A63EC123FF17 CRC64;


  Query Match             15.9%;  Score 280.5;  DB 4;  Length 502;
  Best Local Similarity   27.8%;  Pred. No. 5.7e-19;
  Matches   88;  Conservative   51;  Mismatches  138;  Indels   39;  Gaps   11;

Qy      20 LLLLNVLAPGR-ASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNIYI 78
           |:|::: |  | | ||    |  | |          |     |:  :| |   ::: :
Db       3 LVLISLAALCRSAVPR---EPTVQCGSE---------TGPSPEWMLQHDLIPGDLRDLRV 50

Qy      79 NLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL-QLNTNERLCVKFQFLSMLQH 137
             :|   |:   :::| | |: |||| |:  :: |  : |     ||:  :    |
Db      51 EPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQT 110

Qy     138 HRK----RWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMKMT 193
           :    :| ||:  | |:    | :  |::|    : |     |       | | |  ||
Db     111 QTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170

Qy     194 TSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIF 253
             || :|||||||||    : : : |:||       |  |::       ||      |:|
Db     171 KKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQ-------HSTIIGFSQVF 223

Qy     254 APRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVP-CPVISNTTVP 312
           | |::   ||:|   ::          ||: |:| :| :||:||  ||  ||    | ||
Db     224 EPHQKK-QTRASVVIPVTGDSEGA--TVQLTPYFPTCGSDCIRHKGTVVLCP---QTGVP 277

Qy     313 KPV-------ADYIPL 321
             |:       ::||
Db     278 FPLDNNKSKPGGWLPL 293


RESULT   5
Q9JIP3
ID   Q9JIP3      PRELIMINARY;      PRT;   499 AA.
AC   Q9JIP3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   IL-17 RECEPTOR HOMOLOG PRECURSOR.
GN   EVI27.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20273223; PubMed=10815801;
RA   Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
RA   Shaughnessy J.D. Jr.;
RT   "Evi27 encodes a novel membrane protein with homology to the IL17
RT   receptor.";
RL   Oncogene 19:2098-2109(2000).
DR   EMBL; AF208108; AAF86049.1; -.
KW   Signal; Receptor.
FT   SIGNAL       1     8        POTENTIAL.
FT   CHAIN        9     499      IL-17 RECEPTOR HOMOLOG.
SQ   SEQUENCE   499 AA;  55617 MW;  C66440430E3C31F3 CRC64;


  Query Match             14.0%;  Score 247.5;  DB 11;  Length 499;
  Best Local Similarity   25.4%;  Pred. No. 9.1e-16;
  Matches   82;  Conservative   50;  Mismatches  140;  Indels   51;  Gaps   10;

Qy      19 LLLLLNVLAPG--RASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNI 76
           :||:| :||     |  ||    |  |  |          |     |:   |||   :::
Db       1 MLLVLLILAASCRSALPR---EPTIQCGSE---------TGPSPEWMVQHTLTPGDLRDL 48

Qy      77 YINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL-QLNTNERLCVKFQFLSML 135
           : |  :|    |   :::: | |: ||||  |:  :: |  : | |   ||:  :
Db      49 QVELVKTSVAAEEFSILMNISWILRADASIRLLKATKICVSGKNNMNSYSCVRCNYTEAF 108

Qy     136 QHHRK----RWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMK 191
           |    :    :| ||:  | |:    | :: |::|    : |     |       | | |  ||
Db     109 QSQTRPSGGKWTFSYVGFPVELSTLYLISAHNIPNANMNEDSPSLSVNFTSPGCLNHVMK 168

Qy     192 MTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLE-----SFSDSENHSCF 246
           |  :|||||||:||    : : : |:||       | :|::      ||    :
Db     169 YKKQCTEAGSLWDPDITACKKNEKMVEVNFTTNPLGNRYTILIQRDTTLGFSRVLENKLM 228

Qy     247 DVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVI 306
           :  |  ||                      ||: |:  :| |||:|   ||   :
Db     229 RT--SVAIPVTEESEGAV---------------VQLTPYLHTCGNDCIRREGTV--VLC 268

Qy     307 SNTTVPKPVAD-------YIPLW 322
           | |: | |  |        ::||:
Db     269 SETSAPIPPDDNRRMLGGWLPLF 291


RESULT   6
Q9NRM5
ID   Q9NRM5      PRELIMINARY;      PRT;   288 AA.
AC   Q9NRM5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   TRUNCATED IL-17 RECEPTOR HOMOLOG PRECURSOR.
GN   EVI27.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20273223; PubMed=10815801;
RA   Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
RA   Shaughnessy J.D. Jr.;
RT   "Evi27 encodes a novel membrane protein with homology to the IL17
RT   receptor.";
RL   Oncogene 19:2098-2109(2000).
DR   EMBL; AF208111; AAF86052.1; -.
KW   Signal; Receptor.
FT   SIGNAL       1     13       POTENTIAL.
FT   CHAIN        14    288      TRUNCATED IL-17 RECEPTOR HOMOLOG.
SQ   SEQUENCE   288 AA;  31773 MW;  CD8EB2C0C235FBFB CRC64;


  Query Match             13.1%;  Score 231;  DB 4;  Length 288;
  Best Local Similarity   25.7%;  Pred. No. 1.9e-14;
  Matches   79;  Conservative   48;  Mismatches  132;  Indels   48;  Gaps   10;

Qy      20 LLLLNVLAPGR-ASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNIYI 78
           |:|::: |  | | ||    |  | |          |     |:   :| |   ::: :
Db       3 LVLISLAALCRSAVPR---EPTVQCGSE---------TGPSPEWMLQHDLIPGDLRDLRV 50

Qy      79 NLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL-QLNTNERLCVKFQFLSMLQH 137
             :|   |:   :::| | |: |||| |:  :: |  : |     ||:  :    |
Db      51 EPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQT 110

Qy     138 HRK----RWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMKMT 193
           :    :| ||:  | |:    | :  |::|    : |     |       | | |  ||
Db     111 QTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170

Qy     194 TSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIF 253
             || :|||||||||    : : : |:||       |  |::       ||      |:|
Db     171 KKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQ-------HSTIIGFSQVF 223

Qy     254 APRQEEFHQRANVTFTL-------------SKFHW-------CCHHHVQVQPFFSSCLND 293
           | |::   ||:|   :             |:  |          || : ::   || |::
Db     224 EPHQKK-QTRASVVIPVTGDSEGATVQVKFSELLWGGKGHRRLFHHSLLLR--MSSLLSN 280

Qy     294 CLRHAVT 300
           |  | |
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Db    281 ALLPADT 287


RESULT   7
Q9JIP2
ID   Q9JIP2      PRELIMINARY;      PRT;   218 AA.
AC   Q9JIP2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   IL-17 RECEPTOR HOMOLOG SHORT ISOFORM PRECURSOR.
GN   EVI27.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20273223; PubMed=10815801;
RA   Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
RA   Shaughnessy J.D. Jr.;
RT   "Evi27 encodes a novel membrane protein with homology to the IL17
RT   receptor.";
RL   Oncogene 19:2098-2109(2000).
DR   EMBL; AF208109; AAF86050.1; -.
DR   InterPro; IPR002259; -.
DR   ProDom; PD005103; -; 1.
KW   Signal; Receptor.
FT   SIGNAL       1      8       POTENTIAL.
FT   CHAIN        9    218       IL-17 RECEPTOR HOMOLOG SHORT ISOFORM.
SQ   SEQUENCE   218 AA;  23855 MW;  E17C154C824E1F0B CRC64;

  Query Match             8.0%;  Score 140.5;  DB 11;  Length 218;
  Best Local Similarity   24.6%;  Pred. No. 8.5e-06;
  Matches   45;  Conservative   32;  Mismatches   87;  Indels   19;  Gaps    5;

Qy      19 LLLLLNVLAPG--RASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNI 76
           :||:| :||     | ||    |   |  |          |     |:    |||   :::
Db       1 MLLVLLILAASCRSALPR---EPTIQCGSE---------TGPSPEWMVQHTLTPGDLRDL 48

Qy      77 YINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL-QLNTNERLCVKFQFLSML 135
           : |  :|    |   :::: | |: ||||  |:  :: |  : | |   ||:  :
Db      49 QVELVKTSVAAEEFSILMNISWILRADASIRLLKATKICVSGKNNMNSYSCVRCNYTEAF 108

Qy     136 QHHRK----RWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMK 191
           |   :    :| ||:  | |:    | :: |::|    : |    |     | |     :
Db     109 QSQTRPSGGKWTFSYVGFPVELSTLYLISAHNIPNANMNEDSPSLSVNFTSPGCTRENTE 168

Qy     192 MTT 194
           :|:
Db     169 VTS 171


RESULT   8
Q9P7H9
ID   Q9P7H9      PRELIMINARY;      PRT;   708 AA.
AC   Q9P7H9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   PUTATIVE TRANSCRIPTIONAL ACTIVATOR.
GN   SPAC105.03C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972H-;
RA   Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL157994; CAB76236.1; -.
DR   InterPro; IPR003015; -.
DR   PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ   SEQUENCE   708 AA;  80989 MW;  78F57C5A0EB2DE76 CRC64;

  Query Match             6.4%;  Score 112.5;  DB 3;  Length 708;
  Best Local Similarity   21.6%;  Pred. No. 0.018;
  Matches   63;  Conservative   45;  Mismatches   78;  Indels  105;  Gaps   15;

Qy      44 AQEGLSCRVKNSTCL-------DDSWIHPKNLTPSSPKNIYINL--------------SV 82
           ||  |       |||           |:: | :|  |||   | ||              ||
Db      14 AQPNLCIPCSLGTCLIHFHEFSSSSFMDPVSLFCSSP---YPNLPPHSRSSSLESKKPSV 70

Qy      83 SS------------TQHGELVPVLHVE---WTLQTDASILYLEGAELSVLQLNTNERLCV 127
           :|            | :  |:|    |   ||:: ::    | |:    :|
Db      71 ASQDVKSDGTLPIGTNNNPLIPSHSQESSHWTIRHESMPSALAGSSAQSMQ--------- 121

Qy     128 KFQFLSMLQHHRK-RWRFSFSHFVVDPGQEYEVTVHHLPKPI------PDGDPNHKSKII 180
             || |: |:    |:: ||:                  |:||      |  :|  :   :
Db     122 --QFPSITQNEENFRFKKSFTQ---------------PQPIVKETTFPKSEPGQEHAKL 163

Qy     181 -------FVPDCEDSKMKMTT------SCVSSGSLWDPNITV----ETLDTQHLRVDFTL 223
                 |:     :|::  :       | ::| :: | | ::      ::| |   ||
Db     164 SDLSYEEFLKKYSSTKVERVSEAAPPPSSLNSSTVLDENDSLISQGSSVDDQ---TDFLG 220

Qy     224 WNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFH 274
           :::|  |  :|   |||:     |:::| | |::          |:| |  |
Db     221 FDDSLSYAYILNPTSDSD----VDLIRQYFIPKEG--------TYTFSNMH 259


RESULT   9
P79927
ID   P79927      PRELIMINARY;      PRT;  1506 AA.
AC   P79927;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   INTEGUMENTARY MUCIN B.1 (FRAGMENT).
GN   FIM-B.1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SKIN;
RX   MEDLINE=97153143; PubMed=8999864;
RA   Joba W., Hoffmann W.;
RT   "Similarities of integumentary mucin B.1 from Xenopus laevis and
RT   prepro-von Willebrand factor at their amino-terminal regions.";
RL   J. Biol. Chem. 272:1805-1810(1997).
DR   EMBL; Y08296; CAA69604.1; -.
DR   HSSP; P19398; 1ATB.
DR   InterPro; IPR000436; -.
DR   InterPro; IPR001846; -.
DR   InterPro; IPR002919; -.
DR   Pfam; PF00084; sushi; 1.
DR   Pfam; PF00094; vwd; 3.
DR   Pfam; PF01826; TIL; 1.
DR   SMART; SM00032; CCP; 1.
FT   NON_TER    1506   1506
SQ   SEQUENCE   1506 AA;  163905 MW;  7BF269A748DC817F CRC64;

  Query Match             5.6%;  Score 99.5;  DB 13;  Length 1506;
  Best Local Similarity   21.1%;  Pred. No. 0.78;
  Matches   63;  Conservative   35;  Mismatches  110;  Indels   91;  Gaps   16;

Qy      56 TCLDDSWIHPKNLTPSSPK---NIYINL--SVSSTQHGELVPV--LHVEW---------- 98
           ||   :|   |   |   |    :|:      :: : ||  | :  :|  |
Db     495 TCNGGTWTCSKGSCPGICKVEEGVYVTTYDGITYSMHGNCVYIISMHTSWLVYAKLSQSQ 554
```

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Qy      99 -----TLQTDASILYLEGAELSVLQLN----------TNERLCVKFQ--------FLSML 135
Db     555 DAQSSTIINSVSLVLNLGNQESTYTFNRDGSIINEKMTNQNVFQSDQLSISRSGTFIIVL 614

Qy     136 QHHRKRWRF----SFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMK 191
Db     615 THLHVNLLIQTGTTMQFYTSVPSTGYEDTEG------PCGSFNHKADDDFM-----SNQK 663

Qy     192 MTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQ 251
Db     664 M-----------PESSPETF------VGF--WK--------MSSCSDPVKPTCIDLEKE 695

Qy     252 IFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLN-DCLRHAVTVP-CPVISN 308
Db     696 LFANQQCSQLKDPNGAFAK------CHSTVLYRSFYERCVHLTCISQDMTVSMCTELRN 748


RESULT  10
Q9IU91
ID   Q9IU91      PRELIMINARY;      PRT;   328 AA.
AC   Q9IU91;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   EXTERIOR MEMBRANE PROTEIN GP120 (FRAGMENT).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=96NG-MACSW031;
RX   MEDLINE=20179113; PubMed=10716369;
RA   Peeters M., Esu-Williams E., Vergne L., Montavon C.,
RA   Mulanga-Kabeya C., Harry T., Ibironke A., Lesage D., Patrel D.,
RA   Delaporte E.;
RT   "Predominance of subtype A and G HIV type 1 in Nigeria, with
RT   geographical differences in their distribution.";
RL   AIDS Res. Hum. Retroviruses 16:315-325(2000).
DR   EMBL; AJ389751; CAB77485.1; -.
DR   InterPro; IPR000777; -.
DR   Pfam; PF00516; GP120; 1.
FT   NON_TER       1      1
FT   NON_TER     328    328
SQ   SEQUENCE   328 AA;  36504 MW;  DE92C03A75CF898E CRC64;


  Query Match             5.5%;  Score 97.5;  DB 14;  Length 328;
  Best Local Similarity   22.2%;  Pred. No. 0.21;
  Matches   70;  Conservative   32;  Mismatches   85;  Indels  129;  Gaps   18;

Qy      20 LLLLNVLAPGRASPRLLDFPAPV--CAQEG---LSCRVKN----STCLDDSWIHPKNLTP 70
Db      64 LINCNVSAINQACPKVSFDPIPIHYCAPAGFAILKCRDKNFNGTGTC------------ 110

Qy      71 SSPKNIYINLSVSSTQ--HGELVPVLHVEWTL-----QTDASIL---YLEGAELSVLQLN 120
Db     111 ---------KIVSTVQCTHG-IKPVVSTQLLLNGSLAEEDIVIRTENYTDNAKIIIVQLN 160

Qy     121 -TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKI 179
Db     161 ETIEINCTRPN-----NNTRKSIRFG-------PGQAFYAT----------GD------- 191

Qy     180 IFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNE---STPYQV-LLE 235
Db     192 ----------------------------IIENIRQAHCNVSRTKWNEMIQKVKVQLRKIE 223

Qy     236 SFS------DSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSS 289
Db     224 SFKNKNISFDSSSGGDLEITTHSFNCRGEFFYCNTSELFTKN----------------ST 267

Qy     290 CLNDCLRHAVTVPCPV 305
```

```
Db     268 SKNST---TITLPCRI 280


RESULT  11
Q9JLN5
ID   Q9JLN5      PRELIMINARY;      PRT;   592 AA.
AC   Q9JLN5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ERYTHROID MEMBRANE-ASSOCIATED PROTEIN ERMAP.
GN   ERMAP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20184753; PubMed=10721728;
RA   Ye T.-Z., Gordon C.T., Lai Y.-H., Fujiwara Y., Peters L.L.,
RA   Perkins A.C., Chui D.H.K.;
RT   "Ermap, a gene coding for a novel erythroid specific adhesion/receptor
RT   membrane protein.";
RL   Gene 242:337-345(2000).
DR   EMBL; AF153906; AAF31162.1; -.
DR   InterPro; IPR000107; -.
DR   InterPro; IPR001211; -.
DR   InterPro; IPR001870; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00622; SPRY; 1.
DR   PRINTS; PR01407; BUTYPHLNCDUF.
DR   ProDom; PD000303; -; 1.
DR   SMART; SM00406; IGv; 1.
SQ   SEQUENCE   592 AA;  66555 MW;  246AC691B8788BE8 CRC64;


  Query Match             5.4%;  Score 94.5;  DB 11;  Length 592;
  Best Local Similarity   21.9%;  Pred. No. 0.8;
  Matches   69;  Conservative   39;  Mismatches  112;  Indels   95;  Gaps   15;

Qy      65 PKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLNTNER 124
Db     263 PERGSLSSPA---VALSV-------VLPVL----------GLLILLGIWLICKQKKSKEK 302

Qy     125 LCVK--FQFLSMLQHHRKR------------------------WRFSFSHFV---VDPG 154
Db     303 LLYEQAMEVESLLEDHAKEKGRLHKALKKLRSELKLKRAAANAGWRRARLHFVAVTLDPD 362

Qy     155 QEYE----------VTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMKMTTSC------VS 198
Db     363 TAHPKLILSEDRRCVRLGDRKRPVPD-NPERFDFVVSVPGSE----YFTTGCHYWEVYVG 417

Qy     199 SGSLWDPNITVETLDTQ----------HLRVDFTLWNESTPYQVLLE---SFSDSENHSC 245
Db     418 EKTKWILGVCSESVSRKGKVTASPANGHWLVRQSRGNE---YEALTSPQTSFRLKESPKC 474

Qy     246 FDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVPCPV 305
Db     475 VG----IFLDYEAGIISFYNVTDKSHIFTFTHSFSSPLRPFFEPCLHDEGKNT----APL 526

Qy     306 ISNTTVPKPVADYIP 320
Db     527 IICTELQKSEESIVP 541


RESULT  12
Q9FX72
ID   Q9FX72      PRELIMINARY;      PRT;   682 AA.
AC   Q9FX72;
```

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DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   F19K19.13 PROTEIN.
GN   F19K19.13.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC   Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA   Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
RA   Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA   Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA   Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC011808; AAG10824.1; -.
SQ   SEQUENCE   682 AA;  77036 MW;  D5713DF18EA87D94 CRC64;

  Query Match             5.2%;  Score 92;  DB 10;  Length 682;
  Best Local Similarity   22.9%;  Pred. No. 1.6;
  Matches   71;  Conservative   36;  Mismatches  109;  Indels   94;  Gaps   17;

Qy      66 KNLTPS------SPKNIYINLSVSSTQHGE--LVPVLHVEWTLQ---------------- 101
           |:||||      : :||:   : : :||    | ||:    |:
Db     269 KSLTPSAIWMHTTSLSIYVKKKLQALRHGNGAAVCVLYGSENLELSSHKSGPTVTFNLKR 328

Qy     102 TDASIL-YLEG---AELSVLQLNTNERLC----------------VKFQFLSMLQHHRKR 141
             | |   |||    | || :||     :|                | | ::|  :  :|
Db     329 PDGSWFGYLEVEKLASLSGIQLRAG-HICWDDNDVINGKPTGAVRVSFGYMSTFEDAKKF 387

Qy     142 WRFSFSHFVVDPGQEYEVTV--HHLPKPIPDGD-------PNHKSKIIFV---PDCEDSK 189
             |  | |   | :    ||     |: :|  |       |:|  | | |     |
Db     388 IDFIISSFASPPKKTGNGTVVSGRFPQ-LPSEDLESKESFPSHYLKSITVYPIKSCAGFS 446

Qy     190 MKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSD-------SEN 242
           :     |  :| | |    |: |  :       |  :  |  |:::| |          |:
Db     447 VIRWPLC-RTGLLHDREWMVQGLTGE------ILTQKKVPEMSLIKTFIDLEEGLLSVES 499

Qy     243 HSCFD-----VVKQIFAPRQEEFHQRANVT------------FTLSKFHWCCHHHVQVQP 285
             | |     :    : || :||   ||:             || :    |     ::
Db     500 SRCEDKLHIRIKSDSYNPRNDEFDSHANILENRNEETRINRWFTNAIGRQC-----KLLR 554

Qy     286 FFSSCLNDCL 295
           : ||   |||
Db     555 YSSSTSKDCL 564


RESULT  13
O42926
ID   O42926      PRELIMINARY;      PRT;  3131 AA.
AC   O42926;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
DE   VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN.
GN   SPBC16C6.02C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972H-;
RA   Purnelle B., Goffeau A., Wood V., Lyne M., Rajandream M.A.,
RA   Barrell B.G.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL021767; CAA16910.1; -.
SQ   SEQUENCE   3131 AA;  354021 MW;  BBD22BE7F668EEF4 CRC64;

  Query Match             5.2%;  Score 91.5;  DB 3;  Length 3131;
  Best Local Similarity   20.6%;  Pred. No. 11;
  Matches   68;  Conservative   54;  Mismatches  125;  Indels   83;  Gaps   15;

Qy      17 GWLLLLLNVLAPGRASP----------RLLDF----PAPVCAQEGLSCRVKNSTCLDDSW 62
           |:: | |  | | |  |          :::|:     :|:   : |:|   :::   :
Db    1898 GYVPLDLACLYPLRIRPVSKLGFLWSNQIVDWHSLNKSPL---QYLTCESTSTSWKHNLL 1954

Qy      63 IHPKNLTPSSPKNIY--------------------INLSV----------SSTQHGELVP 92
           :  :||   | :| |                    ||| :          ||   |: :|
Db    1955 VFARNLMDGSLQNDYPFLQLNILPTLQIENLLPYEINLRIIERSSGNDWRSSLSPGDSLP 2014

Qy      93 VLHV-------------EWTLQ-TDASILYL---EGAELSVLQLNTNE------RLCVKF 129
           :||               :  ||  |  |:|     | ::    | |        :| :|:
Db    2015 ILHTDSKSFLLMGINVPDLDLQPVDLPIIYTPISSGQDVQTSALLTASDKQDVVKLILKY 2074

Qy     130 QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTV-----HHLPKPIPDGDPNHKSKIIFVPD 184
           : |    :  |     :  :|:    :  : |     : :   || |  ::  |  |
Db    2075 EKLPGTNYVSK--VMIYPPYVIFNHTDLSIQVTSSSPNSIRYTIPSGSYSNDIKPYFYSF 2132

Qy     185 CEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
           |  :      : :|: |  :|  :|| :   :|:    |||    | |   | ||:
Db    2133 DESGRKNRAMISIDNGTSWSADIGFDTLGSSS-QVEVRKTNES---DVCLLGMSISESSG 2188

Qy     245 CFDVVKQI-FAPRQEEFHQRANVTFTLSKF 273
           | : | : | ||   |    : | :| :|
Db    2189 KFCLTKSVTFTPR-FVFKNHLDCTVSLREF 2217


RESULT  14
O62453
ID   O62453      PRELIMINARY;   PRT;   333 AA.
AC   O62453;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE   Y44A6C.2 PROTEIN.
GN   Y44A6C.2.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ainscough R.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA   Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA   Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA   Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA   Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
DR   EMBL; AL021489; CAA16370.1; -.
SQ   SEQUENCE   333 AA;  38801 MW;  8B6CC20CE156DFBC CRC64;

  Query Match             5.2%;  Score 91;  DB 5;  Length 333;
  Best Local Similarity   20.2%;  Pred. No. 0.89;
  Matches   59;  Conservative   44;  Mismatches  105;  Indels   84;  Gaps   13;
```

```
Qy      50 CRVKNSTCLD---------DSWIHP----KNLTPSSPKNIYINLSVSSTQHGELVPVLHV 96
           | |  :| ||      .      |||         | |:: :   :   :        :  :| :
Db      50 CDVSENTSLDYRSNHQQLLKSWISSTEKIAQLFPTTLRTFQVTPPM-------IAAILDL 102

Qy      97 EWTLQTDASILYLEG---AELSVLQLNTNERLCVKFQFL-------SMLQHHRKRWRFSF 146
           |  :      :| ::    ||:   | : :        ||:         :: || : :  |
Db     103 ETAIPKTCDVLIIQNYVPAEMDRYQESVD-------QFMEKCHIREGVVLHH-EVYTNSP 154

Qy     147 SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFV--PDCEDSKMKMTTSCVSSGS--- 201
             | :|       ::| |     :|       ::||:::    |  || |       : |||
Db     155 KMFQLD-----YLSVTHSDWMVPSDLEEMENKIVYLDKSDFYDSDMNQFLRELKSGSSHS 209

Qy     202 --------------LWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFD 247
                         |||:  :| |: :       |||::   |      | ::|:   |
Db     210 RLQILSIQGNSWQNYWDPSDVLEGLNAE-------LWNQTERNQ---HYFLNAEHRKNFK 259

Qy     248 VVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAV 299
            :   | | ||:             |     | | :   |    ||  | :|
Db     260 KIADHFYPDQED-----------GFGAELEHGVDLSEAFDFLKNDGTRVSV 299
```

RESULT 15
Q22531
ID Q22531 PRELIMINARY; PRT; 1815 AA.
AC Q22531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE T16G12.1 PROTEIN.
GN T16G12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z30317; CAA82971.2; -.
DR InterPro; IPR000130; -.
DR InterPro; IPR001117; -.
DR InterPro; IPR001930; -.
DR Pfam; PF01433; Peptidase_M1; 3.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_2.
SQ SEQUENCE 1815 AA; 207455 MW; 73EF51E9CA0359E9 CRC64;

Query Match 5.1%; Score 89.5; DB 5; Length 1815;
Best Local Similarity 21.2%; Pred. No. 9;
Matches 65; Conservative 44; Mismatches 108; Indels 89; Gaps 15;

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Qy      28 PGRASPRLLDFP----------------------APVCAQEGLSCRVKNSTCLDDSWIHP 65
           || | | : | |                      |   |||||           |::
Db    1380 PGVAKPVISDTPPVFGIEPYYKGSALLNLLNNVLTPAVFQEGLS-----------SYLTQ 1428

Qy      66 KNLTPSSPKNIYINLSVSSTQH------GELVPVLHV--EWTLQTDASILYLEGAELSVL 117
                :||:|:: :|:|:: :|      |: : |      :||||   |: |     | :
Db    1429 YGYVNASPRNLWTSLTVAAQRHNITDWNGQPLDVSSFMDPYTLQTSYPIITLTLRGTSTV 1488

Qy     118 QLNTNERLCVKFQFLSMLQHHRKRWR----------FSFSHFVVDPGQEYEVTVHHLPKP 167
           |   |:: |:  : |          |              |: ||   |      :    :|
Db    1489 Q--ANQQSCMSDETL---------WNVPLFTQTPGALDFNWFVNFTGGNDATWL----RP 1533

Qy     168 IPDG-----------DPNHKSKIIFVPDCE-DSKMKMTTSCVSSGSLWDPNITVETLDT 214
           :| |              |:  |  :    :  | |   :|   :  | | |  ::
Db    1534 LPTGYRVDNAGSTSFARINYDDKSWYSIQAQLLSNMNTMSSTTRAMLLDDANFFYQSGRW 1593

Qy     215 QHLR-VDFTLW--NEST--PYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFT 269
           :  : :| ||: ||  :  |::  :| |::  |   |    :|   |        |
Db    1594 EMTKFLDLTLYLVNEDSLAPWEQAIEFFTEMLNR--FQYQPEIDTVRNYVIQITKN---A 1648
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Qy     270 LSKFHW 275
           :||| |
Db    1649 VSKFQW 1654
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Search completed: July 17, 2001, 11:20:41
Job time: 160 sec

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:18:26 ; Search time 16.71 Seconds
(without alignments)
660.100 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCWPRVVPGPALGWLL.....CPVISNTTVPKPVADYIPLW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	101	5.7	880	1	TYO3_RAT	P55146 rattus norv
2	99	5.6	449	1	GAD_MOUSE	P22933 mus musculu
3	98	5.5	1748	1	YNR2_YEAST	P53886 saccharomyc
4	97	5.5	880	1	TYO3_MOUSE	P55144 mus musculu
5	95	5.4	449	1	GAD_RAT	P18506 rattus norv
6	94	5.3	388	1	GMCR_MOUSE	Q00941 mus musculu
7	89.5	5.1	606	1	PF20_CHLRE	P93107 chlamydomon
8	88.5	5.0	954	1	YB79_YEAST	P38138 saccharomyc
9	87	4.9	452	1	GAD_HUMAN	O14764 homo sapien
10	87	4.9	520	1	CPF2_HUMAN	P78329 homo sapien
11	87	4.9	2515	1	TUD_DROME	P25823 drosophila
12	86.5	4.9	377	1	ICE4_HUMAN	P49662 homo sapien
13	86	4.9	2569	1	LMA3_MOUSE	Q61789 mus musculu
14	85.5	4.8	1164	1	DP3A_VIBCH	P52022 vibrio chol
15	85	4.8	925	1	DBL_HUMAN	P10911 homo sapien
16	84.5	4.8	429	1	EPC_RAT	P01855 rattus norv
17	84.5	4.8	455	1	ZPR1_CAEEL	O16999 caenorhabdi
18	83.5	4.7	1213	1	T2D2_DROME	Q24325 drosophila
19	83	4.7	432	1	BRAC_XENLA	P24781 xenopus lae
20	83	4.7	672	1	KPCA_HUMAN	P17252 homo sapien
21	83	4.7	672	1	KPCA_RABIT	P10102 oryctolagus
22	83	4.7	672	1	KPCA_RAT	P05696 rattus norv
23	83	4.7	1038	1	ITA4_HUMAN	P13612 homo sapien
24	82.5	4.7	329	1	GCC_RAT	P20762 rattus norv
25	82	4.6	672	1	KPCA_BOVIN	P04409 bos taurus
26	82	4.6	808	1	POLG_HPAVG	Q02381 hepatitis a
27	82	4.6	852	1	POLG_HPAVC	P06442 hepatitis a
28	81.5	4.6	1134	1	IF3X_HUMAN	O75153 homo sapien
29	81.5	4.6	1152	1	ITAM_HUMAN	P11215 homo sapien
30	81	4.6	510	1	VL1_HPV22	P50788 human papil
31	81	4.6	672	1	KPCA_MOUSE	P20444 mus musculu
32	81	4.6	839	1	POLG_HPAVT	P31788 simian hepa
33	80.5	4.6	421	1	EPC_MOUSE	P06336 mus musculu
34	80.5	4.6	2347	1	KROS_HUMAN	P08922 homo sapien
35	80	4.5	666	1	ZP2_RABIT	P48829 oryctolagus
36	79.5	4.5	392	1	BM15_HUMAN	O95972 homo sapien
37	79.5	4.5	658	1	KPC1_LYTPI	Q25378 lytechinus
38	79.5	4.5	716	1	ZP2_PIG	P42099 sus scrofa
39	79	4.5	488	1	PHR_SYNY3	Q55081 synechocyst
40	79	4.5	745	1	ZP2_MACRA	O77726 macaca radi
41	79	4.5	887	1	MCM2_DROME	P49735 drosophila
42	79	4.5	3418	1	BRC2_HUMAN	P51587 homo sapien
43	79	4.5	3712	1	LMA_DROME	Q00174 drosophila
44	78.5	4.4	377	1	ICED_HUMAN	O75601 homo sapien
45	78.5	4.4	450	1	COPP_MOUSE	O55029 mus musculu

ALIGNMENTS

```
RESULT   1
TYO3_RAT
ID   TYO3_RAT       STANDARD;      PRT;   880 AA.
AC   P55146;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (EC 2.7.1.112)
DE   (TYROSINE-PROTEIN KINASE SKY).
GN   TYRO3 OR SKY.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96104999; PubMed=7490270;
RA   Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.;
RT   "Molecular cloning and in situ localization in the brain of rat sky
RT   receptor tyrosine kinase.";
RL   J. Biochem. 117:1267-1275(1995).
CC   -!- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
CC       IN THE CENTRAL NERVOUS SYSTEM.
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
CC       OTHER TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
CC       AXL/UFO SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D37880; BAA07119.1; -.
DR   HSSP; P11362; 1FGI.
DR   InterPro; IPR000719; -.
DR   InterPro; IPR001245; -.
DR   InterPro; IPR001777; -.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW   Transferase; Phosphorylation; Transmembrane; Signal; Repeat;
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KW   Immunoglobulin domain.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    880       TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
FT   DOMAIN       31    419       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    420    440       POTENTIAL.
FT   DOMAIN      441    880       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       47    114       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      143    200       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      214    301       FIBRONECTIN TYPE-III.
FT   DOMAIN      305    401       FIBRONECTIN TYPE-III.
FT   DOMAIN      508    785       PROTEIN KINASE.
FT   NP_BIND     514    522       ATP (BY SIMILARITY).
FT   BINDING     540    540       ATP (BY SIMILARITY).
FT   ACT_SITE    645    645       BY SIMILARITY.
FT   DISULFID     54    107       BY SIMILARITY.
FT   DISULFID    150    193       BY SIMILARITY.
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     75     75       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    220    220       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    230    230       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    283    283       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    356    356       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    370    370       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     676    676       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ   SEQUENCE   880 AA;  95918 MW;  C3751E86AAE5FA5B CRC64;


  Query Match             5.7%;  Score 101;  DB 1;  Length 880;
  Best Local Similarity   21.4%;  Pred. No. 0.75;
  Matches   78;  Conservative   53;  Mismatches  129;  Indels  104;  Gaps   19;

Qy       1 MAIRRCWPRVVPGPALGWLLL--LLNVLAPGRASP--RLLDFPAPVCAQEG----LSCRV 52
           ||:||   |    | |  |||  | ::| || |:   :|:  |  :  :|    |:| |
Db       1 MALRRSMGR----PGLRPLLLAGLASLLLPGSAAAGLKLMGAPVKMTVSQGQPVKLNCSV 56

Qy      53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGA 112
           :     |  |:    :  :: :   :::|:|       : :| ::   ::|| : : :
Db      57 EGMDDPDIHWMKDGAVVQNASQ---VSISISEQ---NWIGLLSLKSAERSDAGLYWCQVK 110

Qy     113 ELSVLQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDP-----------------G 154
           :   ::: :  | |:                    | |:|                   |
Db     111 DGEETKISQSVWLTVE---------------GVPFFTVEPKDLAVPPNVPFQLSCEAVG 154

Qy     155 QEYEVTVHHLPKPIPDGDPNHKSKIIFVP--------DCEDSKMK-MTTSCVSSGSLWDP 205
           ||:     |   | |    :: |          ||   :| : ||  :   |  |
Db     155 PPEPVTIFWWRGPTKVGGPASSPSVLNVTGVTQRTEFSCEAHNIKGLATSRPAIIRLQAP 214

Qy     206 -----NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQEEF 260
                |||| |: : :  |    |        ||        |||   |:   ||   |:
Db     215 PAAPFNITVTTISSSNASV---AWVPGADGLALL--------HSC--TVQVAHAP--GEW 259

Qy     261 HQRANVTFTLSKFHWCCHHHVQVQPFFSSC----LNDCLRHAVTVPCPVISNTTVPKPVA 316
             | |               | | ||  :|    |     ::: | |   :|   | |
Db     260 EALAVV-------------VPVPPF--TCLLRNLAPATNYSLRVRC---ANALGPSPYG 300

Qy     317 DYIP 320
           |::|
Db     301 DWVP 304


RESULT   2
GAD_MOUSE
ID   GAD_MOUSE      STANDARD;      PRT;   449 AA.
AC   P22933;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91103876; PubMed=2176788;
RA   Sommer B., Poustka A., Spurr N.K., Seeburg P.H.;
RT   "The murine GABAA receptor delta-subunit gene: structure and
RT   assignment to human chromosome 1.";
RL   DNA Cell Biol. 9:561-568(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2J; TISSUE=Brain;
RX   MEDLINE=92370453; PubMed=1324097;
RA   Wang J.B., Kofuji P., Burt D.R.;
RT   "Strain comparisons and developmental profile of the delta subunit of
RT   the murine GABAA receptor.";
RL   Brain Res. Bull. 29:119-123(1992).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60596; AAA37652.1; -.
DR   EMBL; M60587; AAA37652.1; JOINED.
DR   EMBL; M60588; AAA37652.1; JOINED.
DR   EMBL; M60589; AAA37652.1; JOINED.
DR   EMBL; M60591; AAA37652.1; JOINED.
DR   EMBL; M60592; AAA37652.1; JOINED.
DR   EMBL; M60593; AAA37652.1; JOINED.
DR   EMBL; M60594; AAA37652.1; JOINED.
DR   EMBL; M60595; AAA37652.1; JOINED.
DR   EMBL; S42882; AAB22967.1; -.
DR   PIR; A36303; A36303.
DR   MGD; MGI:95622; Gabrd.
DR   InterPro; IPR000188; -.
DR   InterPro; IPR001175; -.
DR   Pfam; PF00065; neur_chan; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL        1     16
FT   CHAIN        17    449       GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA
FT                                 SUBUNIT.
FT   DOMAIN       17    248       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    249    271       PROBABLE.
FT   TRANSMEM    275    297       PROBABLE.
FT   TRANSMEM    309    331       PROBABLE.
FT   DOMAIN      332    426       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    427    449       PROBABLE.
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    164    178       BY SIMILARITY.
FT   CONFLICT    255    255       Y -> H (IN REF. 2).
SQ   SEQUENCE   449 AA;  50522 MW;  C00BCA1C3322BF19 CRC64;


  Query Match             5.6%;  Score 99;  DB 1;  Length 449;
  Best Local Similarity   22.5%;  Pred. No. 0.48;
  Matches   64;  Conservative   44;  Mismatches   84;  Indels   92;  Gaps   17;
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Qy      16 LGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKN------STCLDDSWI------ 63
           ||||||           | ||     :| |     |  |       : |: ||:
Db       4 LGWLLL-----------PLLL-----LCTQPHHGARAMNDIGDYVGSNLEISWLPNLDGL 47

Qy      64 ---HPKNLTP---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL 117
              : :|  |    :| |: : | |:|  |   :   ::|:|:      |:    :  :
Db      48 MEGYARNFRPGIGGAPVNVALALEVASIDH---ISEANMEYTMTV---FLHQSWRDSRLS 101

Qy     118 QLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQE--YEVTVHH-LPKPIPDGDPN 174
           :||| | :  :|:  |        :    |:|:     ::||| : | :  |||
Db     102 YNHTNETLGLDSRFVDKL--------WLPDTFIVNAKSAWFHDVTVENKLIRLQPDG--- 150

Qy     175 HKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLL 234
               |::       ::  | :|       | ::    || |   :|             |
Db     151 ---VILY-----SIRITSTVAC-------DMDLAKYPLDEQECMLD-------------L 182

Qy     235 ESFSDSENHSCFDVVKQIFAPRQEEFH-----QRANVTFTLSKF 273
           ||:     :|  |:|   ::  ||: |     | |  | |  :|
Db     183 ESY----GYSSEDIV-YYWSENQEQIHGLDRLQLAQFTITSYRF 221


RESULT   3
YNR2_YEAST
ID   YNR2_YEAST     STANDARD;      PRT;  1748 AA.
AC   P53886;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   HYPOTHETICAL 196.1 KDA PROTEIN IN RPS3-PSD1 INTERGENIC REGION.
GN   YNL172W OR N1677.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Obermaier B., Piravandi E., Rinke M., Domdey H.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO A.NIDULANS BIME AND MOUSE TSG24.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; Z71448; CAA96060.1; -.
DR   SGD; S0005116; YNL172W.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM   1378   1398       POTENTIAL.
SQ   SEQUENCE   1748 AA;  196142 MW;  34BC9212020BB2B5 CRC64;


  Query Match             5.5%;  Score 98;  DB 1;  Length 1748;
  Best Local Similarity   22.9%;  Pred. No. 3.1;
  Matches   69;  Conservative   38;  Mismatches  104;  Indels   90;  Gaps   16;

Qy      29 GRASPRLLDFPAP-VCAQEGLSC---RVKNSTCLDDSWIHPKNLTPSSPKNIYINLSVSS 84
           | || |   |  |  |::  ||    |: |:       | | |   ::|   : : | ::
Db     289 GNASGRTDIFALPSSCSRRSLSATLDRMGNN-------IAPTN--RAAPSGFFDSSSANT 339

Qy      85 TQHGELVPV-------LHVEWTLQTDASILYLEGAELSVLQLN-----TNERL---CVKFQ 130
             |  : ||         |:  ||  |   :   |:| |:|      |: ||     | :
Db     340 ATHSNITPVSQPMQQQQQEYLNQTATSSKDIVLTEISSLKLPDDIIFTSRRLSSILSKLK 399

Qy     131 FLSML------------QHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKS 177
           |||:              |  | |      |:|          :|  |    | :
Db     400 FLSLRFERREGLLIFHEPTHFCKIWLIDLLPDVLD----------SIPFKIYGNSPQNMI 449

Qy     178 KIIFVPDCEDSKMK-----------MTTSC---VSSGS--------LWDPNITVETLDT 214
           ::      |: |:|            :  ||   || |         |:|| : : |  :
Db     450 RL------ENLKLKEPSRIQAMYIHELLESCLILVSEGQNKEEYKACLYDPFVKI-TSPS 502

Qy     215 QHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFH 274
           :::  : |  |     | |       |    ||: || | :|         |::|    |
Db     503 KNISEELTKQNSLPSLQKLFPYPETSFTKLCFEAVKYITSP-------AFNISFI---FL 552

Qy     275 W 275
           |
Db     553 W 553


RESULT   4
TYO3_MOUSE
ID   TYO3_MOUSE     STANDARD;      PRT;   880 AA.
AC   P55144;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (EC 2.7.1.112)
DE   (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).
GN   TYRO3 OR DTK OR RSE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94193774; PubMed=7511603;
RA   Mark M.R., Scadden D.T., Wang Z., Gu Q., Goddard A., Godowski P.J.;
RT   "RSE, a novel receptor-type tyrosine kinase with homology to Axl/Ufo,
RT   is expressed at high levels in the brain.";
RL   J. Biol. Chem. 269:10720-10728(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95161079; PubMed=7857657;
RA   Crosier P.S., Lewis P.M., Hall L.R., Vitas M.R., Morris C.M.,
RA   Beier D.R., Wood C.R., Crosier K.E.;
RT   "Isolation of a receptor tyrosine kinase (DTK) from embryonic stem
RT   cells: structure, genetic mapping and analysis of expression.";
RL   Growth Factors 11:125-136(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=94336210; PubMed=8058320;
RA   Lai C., Gore M., Lemke G.;
RT   "Structure, expression, and activity of Tyro 3, a neural adhesion-
RT   related receptor tyrosine kinase.";
RL   Oncogene 9:2567-2578(1994).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Brain;
RX   MEDLINE=95240399; PubMed=7723626;
RA   Schulz N., Paulhiac C., Lee L., Zhou R.;
RT   "Isolation and expression analysis of tyro3, a murine growth factor
RT   receptor tyrosine kinase preferentially expressed in adult brain.";
RL   Brain Res. Mol. Brain Res. 28:273-280(1995).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Brain;
RA   Sasaki M.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
CC       IN THE CENTRAL NERVOUS SYSTEM.
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
CC       OTHER TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
CC       AXL/UFO SUBFAMILY.
```

```
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U05683; AAA19237.1; -.
DR   EMBL; U18933; AAC52148.1; -.
DR   EMBL; X78103; CAA54995.1; ALT_INIT.
DR   EMBL; U18342; AAB26942.1; ALT_INIT.
DR   EMBL; AB000828; BAA19193.1; -.
DR   HSSP; P11362; 1FGI.
DR   MGD; MGI:104294; Tyro3.
DR   InterPro; IPR000719; -.
DR   InterPro; IPR001245; -.
DR   InterPro; IPR001777; -.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW   Transferase; Phosphorylation; Transmembrane; Signal; Repeat;
KW   Immunoglobulin domain.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    880       TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
FT   DOMAIN       31    419       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    420    440       POTENTIAL.
FT   DOMAIN      441    880       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       47    114       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      143    200       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      214    301       FIBRONECTIN TYPE-III.
FT   DOMAIN      305    401       FIBRONECTIN TYPE-III.
FT   DOMAIN      508    785       PROTEIN KINASE.
FT   NP_BIND     514    522       ATP (BY SIMILARITY).
FT   BINDING     540    540       ATP (BY SIMILARITY).
FT   ACT_SITE    645    645       BY SIMILARITY.
FT   DISULFID     54    107       BY SIMILARITY.
FT   DISULFID    150    193       BY SIMILARITY.
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     75     75       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    220    220       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    230    230       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    283    283       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    356    356       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    370    370       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     676    676       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   CONFLICT    630    630       A -> R (IN REF. 3).
FT   CONFLICT    811    811       L -> V (IN REF. 3).
SQ   SEQUENCE   880 AA;  96222 MW;  3B7AC36CB016B3F7 CRC64;


  Query Match             5.5%;  Score 97;  DB 1;  Length 880;
  Best Local Similarity   21.0%;  Pred. No. 1.6;
  Matches   77;  Conservative   55;  Mismatches  126;  Indels  108;  Gaps   20;

Qy       1 MAIRRC--WPRVVPGPALGWLLL--LLNVLAPGRASP--RLLDFPAPVCAQEG----LSC 50
           ||:||   || : |      |||  | ::| || |:   :|:  |  :   :|    |:|
Db       1 MALRRSMGWPGLRP------LLLAGLASLLLPGSAAAGLKLMGAPVKMTVSQGQPVKLNC 54

Qy      51 RVKNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLE 110
             |:     |  |:    :  :: :     :|:| ::|   : :| ::   ::|| : : :
Db      55 SVEGMEDPDIHWMKDGTVVQNASQ-----VSISISEH-SWIGLLSLKSVERSDAGLYWCQ 108

Qy     111 GAELSVLQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDP----------------- 153
             :    ::: :  | |:                    | |:|
Db     109 VKDGEETKISQSVWLTVE----------------GVPFFTVEPKDLAVPPNAPFQLSCEA 152

Qy     154 -GQEYEVTVHHLPKPIPDGDPNHKSKIIFVP--------DCEDSKMK-MTTSCVSSGSLW 203
            |    ||::        | |      :: |          ||   :| : ||  :   |
Db     153 VGPPEPVTIYWWRGLTKVGGPAPSPSVLNVTGVTQRTEFSCEARNIKGLATSRPAIVRLQ 212

Qy     204 DP-----NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQE 258
           |      | || |: : :  |    |         ||         |||   |:   ||
Db     213 APPAAPFNTTVTTISSYNASV---AWVPGADGLALL--------HSC--TVQVAHAP--G 257

Qy     259 EFHQRANVTFTLSKFHWCCHHHVQVQPFFSSC----LNDCLRHAVTVPCPVISNTTVPKP 314
           |:   | |                | | ||  :|    |      ::: | |   :|   | |
Db     258 EWEALAVV-------------VPVPPF--TCLLRNLAPATNYSLRVRC---ANALGPSP 298

Qy     315 VADYIP 320
             |::|
Db     299 YGDWVP 304


RESULT   5
GAD_RAT
ID   GAD_RAT        STANDARD;      PRT;   449 AA.
AC   P18506;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRD.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=90380375; PubMed=2561970;
RA   Shivers B.D., Killisch I., Sprengel R., Sontheimer H., Koehler M.,
RA   Schofield P.R., Seeburg P.H.;
RT   "Two novel GABAA receptor subunits exist in distinct neuronal
RT   subpopulations.";
RL   Neuron 3:327-337(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=90179746; PubMed=1690000;
RA   Zhao Z.Y., Joho R.H.;
RT   "Isolation of distantly related members in a multigene family using
RT   the polymerase chain reaction technique.";
RL   Biochem. Biophys. Res. Commun. 167:174-182(1990).
RN   [3]
RP   ERRATUM.
RA   Zhao Z.Y., Joho R.H.;
RL   Biochem. Biophys. Res. Commun. 168:887-887(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08496; AAC42035.1; -.
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DR   EMBL; M35162; AAA41182.1; -.
DR   PIR; JQ0076; JQ0076.
DR   PIR; A34625; A34625.
DR   InterPro; IPR000188; -.
DR   InterPro; IPR001175; -.
DR   Pfam; PF00065; neur_chan; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL        1     16
FT   CHAIN        17    449       GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA
FT                                 SUBUNIT.
FT   DOMAIN       17    248       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    249    271       PROBABLE.
FT   TRANSMEM    275    297       PROBABLE.
FT   TRANSMEM    309    331       PROBABLE.
FT   DOMAIN      332    426       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    427    449       PROBABLE.
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    164    178       BY SIMILARITY.
SQ   SEQUENCE   449 AA;  50566 MW;  64BDBCDEEB2C70AF CRC64;


  Query Match             5.4%;  Score 95;  DB 1;  Length 449;
  Best Local Similarity   22.2%;  Pred. No. 1;
  Matches   63;  Conservative   44;  Mismatches   85;  Indels   92;  Gaps   17;

Qy      16 LGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKN------STCLDDSWI------ 63
           ||||||           | ||     :| |      |  |        : |: ||:
Db       4 LGWLLL-----------PLLL-----LCTQPHHGARAMNDIGDYVGSNLEISWLPNLDGL 47

Qy      64 ---HPKNLTP---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL 117
              : :|  |     | |: : | |:|  |   :   ::|:|:      |:    :  :
Db      48 MEGYARNFRPGIGGPPVNVALALEVASIDH---ISEANMEYTMTV---FLHQSWRDSRLS 101

Qy     118 QLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQE--YEVTVHH-LPKPIPDGDPN 174
           :||| | :  :|:  |        :    |:|:      ::||| : | :  |||
Db     102 YNHTNETLGLDSRFVDKL--------WLPDTFIVNAKSAWFHDVTVENKLIRLQPDG--- 150

Qy     175 HKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLL 234
           |::       ::  | :|       | ::    :| |   :|              |
Db     151 ---VILY-----SIRITSTVAC-------DMDLAKYPMDEQECMLD-----------L 182

Qy     235 ESFSDSENHSCFDVVKQIFAPRQEEFH-----QRANVTFTLSKF 273
           ||:     :|  |:|   ::  ||: |     | |  | |  :|
Db     183 ESY----GYSSEDIV-YYWSENQEQIHGLDRLQLAQFTITSYRF 221


RESULT   6
GMCR_MOUSE
ID   GMCR_MOUSE     STANDARD;      PRT;   388 AA.
AC   Q00941;
DT   01-OCT-2000 (Rel. 40, Created)
DT   01-OCT-2000 (Rel. 40, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA
DE   CHAIN PRECURSOR (GM-CSF-R-ALPHA) (GMR).
GN   CSF2RA OR CSFGMRA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Neonatal spleen;
RX   MEDLINE=92262426; PubMed=1533931;
RA   Park L.S., Martin U., Sorensen R., Luhr S., Morrissey P.J., Cosman D.,
RA   Larsen A.;
RT   "Cloning of the low-affinity murine granulocyte-macrophage colony-
RT   stimulating factor receptor and reconstitution of a high-affinity
RT   receptor complex.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:4295-4299(1992).
CC   -!- FUNCTION: RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
CC       FACTOR.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN
CC       IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M85078; AAA37421.1; -.
DR   MGD; MGI:1339754; Csf2ra.
DR   InterPro; IPR001777; -.
DR   InterPro; IPR002996; -.
DR   Pfam; PF00041; fn3; 1.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    388       GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
FT                                 FACTOR RECEPTOR ALPHA CHAIN.
FT   DOMAIN       30    327       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    328    348       POTENTIAL.
FT   DOMAIN.     349    388       INTRACELLULAR (POTENTIAL).
FT   CARBOHYD     43     43       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    122    122       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    237    237       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   388 AA;  41798 MW;  8C72E474360770FE CRC64;


  Query Match             5.3%;  Score 94;  DB 1;  Length 388;
  Best Local Similarity   21.6%;  Pred. No. 1.1;
  Matches   68;  Conservative   35;  Mismatches  108;  Indels  104;  Gaps   15;

Qy       5 RCWPR---------------VVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLS 49
           ||| |               | | |  | |  :|  | |  :             | |:
Db      88 RCWFRRMMALHHGVTLDVNGTVGGAAAHWRLSFVNESAAGSGA-------------ENLT 134

Qy      50 CRVKNSTCLDDSWIHPKNLTPSSPKNIYINLSV-SSTQH---------GELVPVLHVEWT 99
           | :: :  |  :|       |::| ::  :| | :|| |         |: |    :
Db     135 CEIRAARFLSCAW----REGPAAPADVRYSLRVLNSTGHDVARCMADPGDDV----ITQC 186

Qy     100 LQTDASILYLEGAELSVLQLNTNERLCVKF-------QFLSML------------QHHRK 140
           :  | |:|   |:|  ::    :    |:|       : |  |             |
Db     187 IANDLSLL---GSEAYLVVTGRSGAGPVRFLDDVVATKALERLGPPRDVTASCNSSHCTV 243

Qy     141 RW--------------RFSFSHFVVDPGQE------YEVTVHHLPKPIPDGDPNHKSKII 180
           |               :|       :||          | |    | | | |    || |:
Db     244 SWAPPSTWASLTARDFQFEVQWQSAEPGSTPRKVLVVEETRLAFPSPAPHG--GHKVKV- 300

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
             |::||           | |   :|  ||   ||   |    |   ||| : :
Db     301 ---RAGDTRMK-------HWGEWSPAHPLEAEDT---RVPGALLYAVTACAVLLCALALG 347

Qy     241 ENHSCFDVVKQIFAP 255
             |:| :::| |
Db     348 VTCRRFEVTRRLFPP 362


RESULT   7
PF20_CHLRE
ID   PF20_CHLRE     STANDARD;      PRT;   606 AA.
AC   P93107;
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DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   FLAGELLAR WD-REPEAT PROTEIN PF20.
GN   PF20.
OS   Chlamydomonas reinhardtii.
OC   Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC   Chlamydomonadaceae; Chlamydomonas.
OX   NCBI_TaxID=3055;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Smith E., Lefebvre P.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBUNIT: INTER-MICROTUBULE BRIDGES IN FLAGELLA.
CC   -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U78547; AAB41727.1; -.
DR   InterPro; IPR001680; -.
DR   Pfam; PF00400; WD40; 7.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   PROSITE; PS00678; WD_REPEATS_1; 4.
DR   PROSITE; PS50082; WD_REPEATS_2; 6.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Repeat; WD repeat; Flagella.
FT   REPEAT      324    354       WD 1.
FT   REPEAT      366    396       WD 2.
FT   REPEAT      408    438       WD 3.
FT   REPEAT      450    480       WD 4.
FT   REPEAT      492    522       WD 5.
FT   REPEAT      534    564       WD 6.
FT   REPEAT      576    606       WD 7.
SQ   SEQUENCE   606 AA;  65839 MW;  7A8779501E3218D1 CRC64;

  Query Match             5.1%;  Score 89.5;  DB 1;  Length 606;
  Best Local Similarity   20.2%;  Pred. No. 4.4;
  Matches   61;  Conservative   34;  Mismatches  118;  Indels   89;  Gaps   13;

Qy      10 VVPGPALGWLLLLLNVLAPGRASPRL-LDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNL 68
           |  ||  ||     :: || | :|   |:|||       |:   |         :   ||
Db     283 VSAGPRSGW----ASLNAPPRRNPYADLEFPAAPVKMLSLNKTFKGHL------LSVANL 332

Qy      69 TPSSPKNIYINLSVSST------QHGELVPV--LHVEWTLQTD----ASILYLEGAELSV 116
             | | :  |   |       |:|:     | :|   |     : |   | : :|
Db     333 ALHPTKPILVTASDDKTWKMWHMPGGDLIMCGEGHKDWVAGVDFHPAGTCLASGGGDSAV 392

Qy     117 LQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHK 176
           :  :: ||     :   | : |   |               ||| : :  |  :|
Db     393 KIWDFEKQRCV----TTFTDHKQAIWSVRF--------------HHLGEVVASGSLDHT 433

Qy     177 SKIIFVPDCEDSKMKM----------------------TTSCVSSGSLWDP--------- 205
           ::  :|     | :|                       | |   : |:||
Db     434 VRLWDLP---AGKCRMALRGHVDSVNDLAWQPFSSSLATASSDKTVSVWDARAGLCTQTY 490

Qy     206 --------NITVETLDTQHLRVD----FTLWNESTPYQV-LLESFSDSENHSCFDVVKQI 252
                 ::   | ||    |      ||:     :|  : :     | ||||   |:
Db     491 YGHQNSCNGVSFNILGTQLASTDADGVVKLWDTRMTAEVATINTGKHPANKSCFDRSGQV 550

Qy     253 FA 254
           |
Db     551 LA 552


RESULT   8
YB79_YEAST
ID   YB79_YEAST     STANDARD;      PRT;   954 AA.
AC   P38138;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   PUTATIVE FAMILY 31 GLUCOSIDASE IN FAT2-PBP2 INTERGENIC REGION
DE   (EC 3.2.1.-).
GN   YBR229C OR YBR1526.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C;
RA   Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A.,
RA   Scherens B., Vierendeels F.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z36098; CAA85192.1; -.
DR   PIR; S46105; S46105.
DR   SGD; S0000433; YBR229C.
DR   InterPro; IPR000322; -.
DR   Pfam; PF01055; Glyco_hydro_31; 1.
DR   PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
DR   PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; FALSE_NEG.
KW   Hypothetical protein; Hydrolase; Glycosidase.
FT   ACT_SITE    537    537       BY SIMILARITY.
SQ   SEQUENCE   954 AA;  110265 MW;  92E93572F04FB009 CRC64;

  Query Match             5.0%;  Score 88.5;  DB 1;  Length 954;
  Best Local Similarity   22.4%;  Pred. No. 9.3;
  Matches   67;  Conservative   43;  Mismatches  102;  Indels   87;  Gaps   18;

Qy      16 LGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKN 75
             | ||:  |         |    |:    ||| |   | :          :: :|:  |   :
Db       4 LKWLVCQLVFFT--AFSHAFTDYLLKKCAQSGFCHRNR---------VYAENIAKS--HH 50

Qy      76 IYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLNTNERLCVKFQF-LSM 134
             |  :   |  |  |  |||    ::|   |  ||| :::            |:| | ||
Db      51 CYYKVDAESIAHDPLENVLHAT-IIKT---IPRLEGDDIA-----------VQFPFSLSF 95

Qy     135 LQHH--------RKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCE 186
           || |         ::|   : |  ::   :  |   :   |   : : |  |    :|
Db      96 LQDHSVRFTINEKERMPTNSSGLLISSQRFNETWKYAFDKKFQE-EANRTS----IPQFH 150

Qy     187 DSKMKMTTSCVSSGSLWDP-----NITVETLDTQHLR---VDFTLWNESTPYQVLL---- 234
             | | | :     | |        :::  | || |||    |   :: |  |:|: :
Db     151 FLKQKQTVN-----SFWSKISSFLSLSNSTADTFHLRNGDVSVEIFAE--PFQLKVYWQN 203

Qy     235 --------ESFSDSENHSCFDVVKQIFAPRQEEFHQRANV-----TFTLSKFHWCCHHH 280
                   ::| : |:|           :|| |   |:|     || : | ::    |
Db     204 ALKLIVNEQNFLNIEHH----------RTKQENF---AHVLPEETTFNMFKDNFLYSKH 249


RESULT   9
GAD_HUMAN
ID   GAD_HUMAN      STANDARD;      PRT;   452 AA.
AC   O14764;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA SUBUNIT PRECURSOR (GABA(A)
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DE   RECEPTOR).
GN   GABRD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Day T.M., Hartnett C., Blankenbiller K., Ramabhadran T.V.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF016917; AAB70007.1; -.
DR   MIM; 137163; -.
DR   InterPro; IPR000188; -.
DR   InterPro; IPR001175; -.
DR   Pfam; PF00065; neur_chan; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL       1    16       POTENTIAL.
FT   CHAIN       17   452       GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA
FT                              SUBUNIT.
FT   DOMAIN      17   248       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM   249   271       PROBABLE.
FT   TRANSMEM   275   297       PROBABLE.
FT   TRANSMEM   309   331       PROBABLE.
FT   DOMAIN     332   429       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM   430   452       PROBABLE.
FT   CARBOHYD   103   103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   106   106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID   164   178       BY SIMILARITY.
SQ   SEQUENCE   452 AA;  50689 MW;  B4696518D39644C4 CRC64;


  Query Match             4.9%;  Score 87;  DB 1;  Length 452;
  Best Local Similarity   22.1%;  Pred. No. 4.9;
  Matches   61;  Conservative   48;  Mismatches   83;  Indels   84;  Gaps   18;

Qy      27 APGR-ASPRLLDFPAPVCAQEGLSCRVKN------STCLDDSWI---------HPKNLTP 70
           || |  :| ||     :|||:    |  |       : |: ||:         : :|  |
Db       3 APARLLAPLLL-----LCAQQLRGTRAMNDIGDYVGSNLEISWLPNLDGLIAGYARNFRP 57

Qy      71 ---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLNTNERLCV 127
                | |: : | |:|  |   :   ::|:|:      |:    :  :   :||| | :
Db      58 GIGGPPVNVALALEVASIDH---ISEANMEYTMTV---FLHQSWRDSRLSYNHTNETLGL 111

Qy     128 KFQFLSMLQHHRKRWRFSFSHFVVDPGQE--YEVTVHH-LPKPIPDGDPNHKSKIIFVPD 184
             :|:  |        :    |:|:      ::||| : | :  |||       |::
Db     112 DSRFVDKL--------WLPDTFIVNAKSAWFHDVTVENKLIRLQPDG------VILY--- 154

Qy     185 CEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
               ::  | :|       | ::    :| |   :|           |||:     :|
Db     155 --SIRITSTVAC-------DMDLAKYPMDEQECMLD------------LESY----GYS 188

Qy     245 CFDVVKQIFAPRQEEFH-----QRANVTFTLSKFHW 275
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           |:|   ::  ||  |     | |   ||:: :|:
Db     189 SEDIV-YYWSESQEHIHGLDKLQLAQ--FTITSYHF 221


RESULT  10
CPF2_HUMAN
ID   CPF2_HUMAN     STANDARD;      PRT;   520 AA.
AC   P78329; Q16677; Q9UIU8; Q9NNZ0;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   CYTOCHROME P450 4F2 (EC 1.14.13.30) (CYPIVF2) (LEUKOTRIENE-B4 OMEGA-
DE   HYDROXYLASE) (LEUKOTRIENE-B4 20-MONOOXYGENASE) (CYTOCHROME P450-
DE   LTB-OMEGA).
GN   CYP4F2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94298958; PubMed=8026587;
RA   Kikuta Y., Kusunose E., Kondo T., Yamamoto S., Kinoshita H.,
RA   Kusunose M.;
RT   "Cloning and expression of a novel form of leukotriene B4 omega-
RT   hydroxylase from human liver.";
RL   FEBS Lett. 348:70-74(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Chen L., Hardwick J.P.;
RT   "The human liver CYP4F2 cDNA sequence and expression in baculovirus-
RT   infected insect cells.";
RL   Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   PubMed=10492403;
RA   Kikuta Y., Miyauchi Y., Kusunose E., Kusunose M.;
RT   "Expression and molecular cloning of human liver leukotriene B4 omega-
RT   hydroxylase (CYP4F2) gene.";
RL   DNA Cell Biol. 18:723-730(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA   Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA   Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA   Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA   Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA   Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA   Kobayashi A., Olsen A.S., Carrano A.V.;
RT   "Sequence analysis of a 1.5 Mb OLFR-rich region in 19p13.1.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1-175 FROM N.A.
RC   TISSUE=Liver;
RX   PubMed=10860554;
RA   Zhang X., Chen L., Hardwick J.P.;
RT   "Promoter activity and regulation of the CYP4F2 leukotriene B4 omega
RT   hydroxylase gene by peroxisomal proliferators and retinoic acid in
RT   HepG2 cells.";
RL   Arch. Biochem. Biophys. 378:364-376(2000).
CC   -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC       MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC       NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC       OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC       ACIDS, AND XENOBIOTICS.
CC   -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC       OXIDIZED FLAVOPROTEIN + H(2)O.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC   -!- TISSUE SPECIFICITY: LIVER.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D26480; BAA05490.1; -.
DR   EMBL; U02388; AAC50052.1; -.
DR   EMBL; AB015306; BAA75823.1; -.
DR   EMBL; AB015295; BAA75823.1; JOINED.
DR   EMBL; AB015296; BAA75823.1; JOINED.
DR   EMBL; AB015297; BAA75823.1; JOINED.
DR   EMBL; AB015298; BAA75823.1; JOINED.
DR   EMBL; AB015299; BAA75823.1; JOINED.
DR   EMBL; AB015300; BAA75823.1; JOINED.
DR   EMBL; AB015301; BAA75823.1; JOINED.
DR   EMBL; AB015302; BAA75823.1; JOINED.
DR   EMBL; AB015303; BAA75823.1; JOINED.
DR   EMBL; AB015304; BAA75823.1; JOINED.
DR   EMBL; AB015305; BAA75823.1; JOINED.
DR   EMBL; AC005336; AAC27730.1; -.
DR   EMBL; AF221943; AAF86378.1; -.
DR   MIM; 604426; -.
DR   InterPro; IPR001128; -.
DR   InterPro; IPR002402; -.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
DR   PRINTS; PR00464; EP450II.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW   Microsome; Endoplasmic reticulum.
FT   BINDING     468    468       HEME (BY SIMILARITY).
FT   CONFLICT     12     12       W -> G (IN REF. 3).
FT   CONFLICT     12     13       WP -> CD (IN REF. 2).
FT   CONFLICT     12     13       WP -> CR (IN REF. 5).
FT   CONFLICT    336    353       GLSWVLYHLAKHPEYQER -> VSPGSCTTLQSTQNTRSV
FT                                (IN REF. 2).
FT   CONFLICT    391    392       LH -> CI (IN REF. 2).
FT   CONFLICT    433    433       V -> M (IN REF. 3).
FT   CONFLICT    488    488       R -> A (IN REF. 2).
FT   CONFLICT    501    517       KPELVLRAEGGLWLRVE -> SRSWSCAQRADFGCGWS
FT                                (IN REF. 2).
SQ   SEQUENCE   520 AA;  59853 MW;  1791F9E6EECB59B5 CRC64;
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  Query Match             4.9%;  Score 87;  DB 1;  Length 520;
  Best Local Similarity   20.0%;  Pred. No. 5.9;
  Matches   61;  Conservative   44;  Mismatches   96;  Indels  104;  Gaps   18;

Qy      60 DSWI-HPKNLTPSSPKNI---YINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAE-L 114
           | |  | : |||:   ||   |: :        | | ::| :| |        |:  | :
Db     142 DKWSRHRRMLTPAFHFNILKPYMKI------FNESVNIMHAKWQLLASEGSACLDMFEHI 195

Qy     115 SVLQLNTNERLCVKFQF----------------LSML---QHHRKRWRFSFSHFVVDPG 154
           |:: |:: :: || | |                || |   :||      | :::   |
Db     196 SLMTLDSLQK-CV-FSFDSHCQEKPSEYIAAILELSALVSKRHHEILLHIDFLYYLTPDG 253

Qy     155 QEY----------EVTVHHLPKPIPDG------DPNHKSK------IIFVPDCEDSKMK 191
           | :          :  :    : :|           |||      :: :   || |
Db     254 QRFRRACRLVHDFTDAVIQERRRTLPSQGVDDFLQAKAKSKTLDFIDVLLLSKDEDGK-- 311

Qy     192 MTTSCVSSGSLWDPNITVET-------LDTQHLRVDFTLWN--ESTPYQVLLESFSDSEN 242
                 | | :|  |          ||    : : |::  :   ||
Db     312 ---------KLSDEDIRAEADTFMFEGHDTTASGLSWVLYHLAKHPEYQ---------- 351

Qy     243 HSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVP 302
           |   |:::   |: :          :  |    |:   || : |: : ||  :  |
Db     352 ERCRQEVQELLKDREPK-----------EIEWDDLAHL---PFLTMCMKESLR--LHPP 394

Qy     303 CPVIS 307
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           ||||
Db     395 VPVIS 399
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RESULT  11
TUD_DROME
ID   TUD_DROME      STANDARD;      PRT;  2515 AA.
AC   P25823;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-AUG-1992 (Rel. 23, Last annotation update)
DE   MATERNAL TUDOR PROTEIN.
GN   TUD.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92038995; PubMed=1936993;
RA   Golumbeski G.S., Bardsley A., Tax F., Boswell R.E.;
RT   "Tudor, a posterior-group gene of Drosophila melanogaster, encodes a
RT   novel protein and an mRNA localized during mid-oogenesis.";
RL   Genes Dev. 5:2060-2070(1991).
CC   -!- FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION OF
CC       PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
CC   -!- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
CC       REGION OF THE DEVELOPING OOCYTE DURING THE EARLY TO MIDDLE STAGES
CC       OF OOGENESIS.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X62420; CAA44286.1; -.
DR   PIR; A41519; A41519.
DR   FlyBase; FBgn0003891; tud.
DR   InterPro; IPR001097; -.
DR   Pfam; PF00567; TUDOR; 10.
KW   Developmental protein.
SQ   SEQUENCE   2515 AA;  285236 MW;  683C100AD308BADA CRC64;
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  Query Match             4.9%;  Score 87;  DB 1;  Length 2515;
  Best Local Similarity   22.6%;  Pred. No. 41;
  Matches   77;  Conservative   50;  Mismatches  119;  Indels   94;  Gaps   20;

Qy      58 LDDSWIHPKNLTPS----------SPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASIL 107
           ||  :   :  |||          ||   ||     | ::  ::  :  |:  |     |
Db    1003 LDKPYALQEMKTPSKEAASLSWWLSPFQFYIVPKSVSAKYDNIMRDMR-EFYRQKQHQPL 1061

Qy     108 YLE-GAELSVLQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVT---VHH 163
            |: |: : | |   |  |      ::   |  :::|     | || |    ||   :
Db    1062 QLKVGSTVVVRQRKDNAILRAT---VTACNHMMRKYRV----FCVDTGSLITVTSEDIWQ 1114

Qy     164 LPKPIPDG---------------DPNHKSKII-----FVP-----DCE-DSKMK----- 191
           | :  |                 || :   |:     |||     |||  || |
Db    1115 LEQRFADPPCMAHRCSFHSVVTNYDPLY---IVDRMETFVPVNAKVDCEFVSKEKSNQGS 1171

Qy     192 -MTTSC-------VSSGSLWD-----------PNITVETLDTQHLRVDFTLWNESTPYQ 231
             :::|       |:  || |            | | |  |  | :|  ||   : | ::
Db    1172 NTSSTCSYTVNIFVNGASLRDMLVKAEFLTEVAPEIRVNLLAGQQIRGKFTSIRDMTSFK 1231

Qy     232 VLLESFSDSENHSC-FDVVKQI-----FAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQP 285
           |  : : :: |  | :|  | :      | | :||::    :| |:  : | :: | ::|
Db    1232 VQFD-YGNNVNFLCTYDDAKFVKSNPNLARRFKEFYE--GKSFALNVKNVCENNIVHLRP 1288
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Qy    286 FFSSCLNDCLRHAVTVPCPVISNT------TVPKPVADYI 319
              : |  | :   | ||: ::         ||   |:
Db   1289 VMPLFMED--RRSFICPYPVVLSSFQALVVYTAKPYRVYV 1326


RESULT  12
ICE4_HUMAN
ID   ICE4_HUMAN     STANDARD;      PRT;   377 AA.
AC   P49662;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX
DE   PROTEASE) (ICE(REL)-II).
GN   CASP4 OR ICH2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., MUTAGENESIS OF C-258, AND 3D-STRUCTURE MODELING.
RC   TISSUE=Placenta;
RX   MEDLINE=95262631; PubMed=7743998;
RA   Faucheu C., Diu A., Chan A.W.E., Blanchet A.-M., Miossec C., Herve F.,
RA   Collard-Dutilleul V., Gu Y., Aldape R.A., Lippke J.A., Rocher C.,
RA   Su M.S.-S., Livingston D.J., Hercend T., Lalanne J.-L.;
RT   "A novel human protease similar to the interleukin-1 beta converting
RT   enzyme induces apoptosis in transfected cells.";
RL   EMBO J. 14:1914-1922(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95318183; PubMed=7797592;
RA   Munday N.A., Vaillancourt J.P., Ali A., Casano F.J., Miller D.K.,
RA   Molineaux S.M., Yamin T.-T., Yu V.L., Nicholson D.W.;
RT   "Molecular cloning and pro-apoptotic activity of ICErelII and
RT   ICErelIII, members of the ICE/CED-3 family of cysteine proteases.";
RL   J. Biol. Chem. 270:15870-15876(1995).
RN   [3]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Thymus;
RX   MEDLINE=95318091; PubMed=7797510;
RA   Kamens J., Paskind M., Hugunin M., Talanian R.V., Allen H., Banach D.,
RA   Bump N.J., Hackett M.C., Johnston C.G., Li P., Mankovich J.A.,
RA   Terranova M., Ghayur T.;
RT   "Identification and characterization of ICH-2, a novel member of the
RT   interleukin-1 beta-converting enzyme family of cysteine proteases.";
RL   J. Biol. Chem. 270:15250-15256(1995).
CC   -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC       RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES CASPASE-1.
CC   -!- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN
CC       SPLEEN AND LUNG. MODERATE EXPRESSION IN HEART AND LIVER, LOW
CC       EXPRESSION IN SKELETAL MUSCLE, KIDNEY AND TESTIS. NOT FOUND IN THE
CC       BRAIN.
CC   -!- PTM: THE TWO SUBUNITS ARE DERIVED FROM THE PRECURSOR SEQUENCE BY
CC       AN AUTOCATALYTIC MECHANISM OR BY CLEAVAGE BY CASPASE-8.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE
CC       CASPASE FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC   -!- CAUTION: THIS PROTEIN COULD BE THE HUMAN ORTHOLOG OF MOUSE
CC       CASPASE-11.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z48810; CAA88750.1; -.
DR   EMBL; U28014; AAA75171.1; -.
DR   EMBL; U25804; AAA86890.1; -.
DR   HSSP; P29466; 1IBC.
DR   MEROPS; C14.007; -.
DR   MIM; 602664; -.
DR   InterPro; IPR001309; -.
DR   InterPro; IPR001315; -.
DR   InterPro; IPR002138; -.
DR   InterPro; IPR002398; -.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00655; ICE_p10; 1.
DR   Pfam; PF00656; ICE_p20; 1.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   PROSITE; PS50209; CARD; 1.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
KW   Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT   PROPEP          1    ?80       POTENTIAL.
FT   CHAIN         ?81    270       CASPASE-4 SUBUNIT 1.
FT   PROPEP        271    289       POTENTIAL.
FT   CHAIN         290    377       CASPASE-4 SUBUNIT 2.
FT   DOMAIN          6     81       CARD.
FT   ACT_SITE      210    210       BY SIMILARITY.
FT   ACT_SITE      258    258
FT   MUTAGEN       258    258       C->S: LOSS OF ACTIVITY.
SQ   SEQUENCE   377 AA;  43262 MW;  DC7CCEC6E9D483EB CRC64;


  Query Match             4.9%;  Score 86.5;  DB 1;  Length 377;
  Best Local Similarity   24.6%;  Pred. No. 4.4;
  Matches   29;  Conservative   13;  Mismatches   33;  Indels   43;  Gaps    6;

Qy    176 KSKIIFVPDCEDSKMKMTTSCVSSGSLW--DPNITVETLDTQ------------HLRVD 220
          | |:| |  |  :         : | ||  |   ::|   :|                |:  |
Db    249 KPKVIIVQACRGA---------NRGELWVRDSPASLEVASSQSSENLEEDAVYKTHVEKD 299

Qy    221 FTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCH 278
          |  :  |||: |   |: ||   | |  : |:                   |: ||||
Db    300 FIAFCSSTPHNV---SWRDSTMGSIF--ITQLIT-------------CFQKYSWCCH 338


RESULT  13
LMA3_MOUSE
ID   LMA3_MOUSE     STANDARD;      PRT;  2569 AA.
AC   Q61789; Q61788; Q61966;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   LAMININ ALPHA-3 CHAIN PRECURSOR (FRAGMENT).
GN   LAMA3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Lung;
RX   MEDLINE=95394948; PubMed=7665604;
RA   Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
RT   "Cloning and complete primary structure of the mouse laminin alpha 3
RT   chain. Distinct expression pattern of the laminin alpha 3A and alpha
RT   3B chain isoforms.";
RL   J. Biol. Chem. 270:21820-21826(1995).
RN   [2]
RP   REVISIONS.
RA   Aberdam D.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 1052-1770 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=94281750; PubMed=8012114;
RA   Aberdam D., Galliano M.-F., Mattei M.-G., Pisani-Spadafora A.,
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RA   Ortonne J.-P., Meneguzzi G.;
RT   "Assignment of mouse nicein genes to chromosomes 1 and 18.";
RL   Mamm. Genome 5:229-233(1994).
RN   [4]
RP   SEQUENCE OF 1052-1770 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=94363405; PubMed=8081888;
RA   Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,
RA   Meneguzzi G.;
RT   "Developmental expression of nicein adhesion protein (laminin-5)
RT   subunits suggests multiple morphogenic roles.";
RL   Cell Adhes. Commun. 2:115-129(1994).
CC   -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
CC       IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC       CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC       WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC   -!- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION
CC       VIA INTEGRIN ALPHA-3/BETA-1 IN FOCAL ADHESION AND INTEGRIN ALPHA-
CC       6/BETA-4 IN HEMIDESMOSOMES, (2) SIGNAL TRANSDUCTION VIA TYROSINE
CC       PHOSPHORYLATION OF PP125-FAK AND P80, (3) DIFFERENTIATION OF
CC       KERATINOCYTES (BY SIMILARITY).
CC   -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC       DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC       TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC       COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC       THE ALPHA-3 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILIGRIN/KALININ/
CC       NICEIN), AND POSSIBLY ALSO A COMPONENT OF LAMININ-6 (K-LAMININ)
CC       AND LAMININ-7 (KS-LAMININ).
CC   -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC       MEMBRANES (MAJOR COMPONENT).
CC   -!- ALTERNATIVE PRODUCTS: THE TWO ISOFORMS A AND B, WHICH DIFFER
CC       IN THEIR N-TERMINAL ARE DERIVED BY ALTERNATIVE SPLICING OF THE
CC       SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF THE LARGER ISOFORM
CC       B.
CC   -!- TISSUE SPECIFICITY: BASAL MEMBRANE OF THE UPPER ALIMENTARY TRACT
CC       AND URINARY AND NASAL EPITHELIA, SALIVARY GLANDS AND TEETH (BOTH
CC       VARIANTS). ISOFORM A IS PREDOMINANTLY EXPRESSED IN SKIN, HAIR
CC       FOLLICLES AND DEVELOPING NEURONS OF THE TRIGEMINAL GANGLION.
CC       ISOFORM B WAS FOUND IN BRONCHI, ALVEOLI, STOMACH, INTESTINAL
CC       CRYPTS, WHISKER PADS, CNS, TELENCEPHALIC NEUROECTODERM, THALAMUS,
CC       RATHKE'S POUCH, AND PERIVENTRICULAR SUBEPENDYMAL GERMINAL LAYER.
CC   -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC       WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC   -!- DOMAIN: DOMAINS IV AND G ARE GLOBULAR.
CC   -!- SIMILARITY: CONTAINS 6.5 LAMININ EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN IV'' IS NOT
CC       SIMILAR TO LAMININ DOMAIN IV).
CC   -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X84014; CAA58837.1; -.
DR   EMBL; X84013; CAA58836.1; -.
DR   EMBL; L20478; AAA68091.1; -.
DR   HSSP; P02468; 1TLE.
DR   MGD; MGI:99909; Lama3.
DR   InterPro; IPR000034; -.
DR   InterPro; IPR000561; -.
DR   InterPro; IPR001791; -.
DR   InterPro; IPR002049; -.
DR   Pfam; PF00052; laminin_B; 1.
DR   Pfam; PF00053; laminin_EGF; 4.
DR   Pfam; PF00054; laminin_G; 3.
DR   PROSITE; PS00022; EGF_1; 4.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 4.
KW   Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW   Laminin EGF-like domain; Cell adhesion; Repeat; Signal;
KW   Alternative splicing.
FT   NON_TER       1      1
FT   SIGNAL       <1     28       POTENTIAL.
FT   CHAIN        29   2569       LAMININ ALPHA-3 CHAIN.
FT   DOMAIN       29    498       DOMAIN IV''.
FT   DOMAIN      499    700       DOMAIN III B.
FT   DOMAIN      546    700       3.5 X LAMININ EGF-LIKE REPEATS.
FT   DOMAIN      546    589       LAMININ EGF-LIKE 1.
FT   DOMAIN      590    639       LAMININ EGF-LIKE 2.
FT   DOMAIN      640    690       LAMININ EGF-LIKE 3.
FT   DOMAIN      691    700       LAMININ EGF-LIKE 4 (N-TERMINAL).
FT   DOMAIN      701    889       LAMININ DOMAIN IV (DOMAIN IV A).
FT   DOMAIN      890   1057       3 X LAMININ EGF-LIKE REPEATS (DOMAIN III
FT                                A).
FT   DOMAIN      890    922       LAMININ EGF-LIKE 4 (C-TERMINAL).
FT   DOMAIN      923    969       LAMININ EGF-LIKE 5.
FT   DOMAIN      970   1022       LAMININ EGF-LIKE 6.
FT   DOMAIN     1023   1057       LAMININ EGF-LIKE 7 (INCOMPLETE).
FT   DOMAIN     1058   1648       DOMAIN II AND I (HEPTAT REPEATS).
FT   DOMAIN     1649   2569       5 X LAMININ G-LIKE REPEATS (DOMAIN G).
FT   DOMAIN     1649   1825       LAMININ G-LIKE 1.
FT   DOMAIN     1826   1994       LAMININ G-LIKE 2.
FT   DOMAIN     1995   2209       LAMININ G-LIKE 3.
FT   DOMAIN     2210   2385       LAMININ G-LIKE 4.
FT   DOMAIN     2386   2569       LAMININ G-LIKE 5.
FT   DOMAIN     1090   1219       COILED COIL (POTENTIAL).
FT   DOMAIN     1251   1296       COILED COIL (POTENTIAL).
FT   DOMAIN     1327   1404       COILED COIL (POTENTIAL).
FT   DOMAIN     1450   1477       COILED COIL (POTENTIAL).
FT   DOMAIN     1557   1622       COILED COIL (POTENTIAL).
FT   SITE       1513   1515       CELL ATTACHMENT SITE (POTENTIAL).
FT   DISULFID    546    553       BY SIMILARITY.
FT   DISULFID    548    560       BY SIMILARITY.
FT   DISULFID    562    571       BY SIMILARITY.
FT   DISULFID    574    587       BY SIMILARITY.
FT   DISULFID    590    605       BY SIMILARITY.
FT   DISULFID    592    612       BY SIMILARITY.
FT   DISULFID    614    623       BY SIMILARITY.
FT   DISULFID    626    637       BY SIMILARITY.
FT   DISULFID    640    652       BY SIMILARITY.
FT   DISULFID    642    659       BY SIMILARITY.
FT   DISULFID    661    670       BY SIMILARITY.
FT   DISULFID    673    688       BY SIMILARITY.
FT   DISULFID    923    932       BY SIMILARITY.
FT   DISULFID    925    939       BY SIMILARITY.
FT   DISULFID    942    951       BY SIMILARITY.
FT   DISULFID    954    967       BY SIMILARITY.
FT   DISULFID    970    982       BY SIMILARITY.
FT   DISULFID    972    991       BY SIMILARITY.
FT   DISULFID    993   1002       BY SIMILARITY.
FT   DISULFID   1005   1020       BY SIMILARITY.
FT   DISULFID   1058   1058       INTERCHAIN (PROBABLE).
FT   DISULFID   1061   1061       INTERCHAIN (PROBABLE).
FT   CARBOHYD    591    591       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    912    912       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1398   1398       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1500   1500       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1571   1571       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1600   1600       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1737   1737       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1819   1819       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1986   1986       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2333   2333       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2509   2509       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1    842       MISSING (IN ISOFORM A).
FT   VARSPLIC    843    901       MTVLPRLERLHIRGLHFTETQRLTLGEVGLEEASDTGSGPR
FT                                AHLVEMCACPPDYTGDSC -> MLPAVRWSAWSTGWLWIFG
FT                                AALGQCLGYGSEQQRVAFLQRPSQNHLQASYMELRPS (IN
FT                                ISOFORM A).
SQ   SEQUENCE   2569 AA;  282159 MW;  40D4306BEF340DBC CRC64;
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  Query Match             4.9%;  Score 86;  DB 1;  Length 2569;
  Best Local Similarity   20.9%;  Pred. No. 51;
  Matches   58;  Conservative   41;  Mismatches  113;  Indels   66;  Gaps   12;

Qy      28 PGRASPRLLDFPA-PVCAQ-EGLSCRV------KNSTCLDDSWIHP-KNLTPSSPKNIYI 78
           ||   || | ||    | : : |: |      | :  |: : : | :      | || :
Db    1780 PGFELPRRLRFPPYKGCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFE 1839

Qy      79 NLSVSSTQHGELVPVLHVEWTLQT--DASILYLEGAELSVLQLNTNE-RLCVKFQ----- 130
           :        |   : ||:||  |  :|:    : : : ||  :  | ||::
Db    1840 GTGYARIPTQPNAPFPKLSWTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVKYKLNSEP 1899

Qy     131 ----------------FLSMLQHHRKRWRFSFS-HFVVDPGQEYEVTVHHL---PKPIP 169
                           |  :   :||   : : | ::  |: :: : ::|   |  |
Db    1900 PKEKGIRDTINNGRDHMILISIGKSQKRMLINMNKHSIIIEGEIFDFSTYYLGGIPIAIR 1959

Qy     170 DGDP------------NHKSKIIFVPD--------CEDSKMKMTTSCVSSGSLWDPNIT 208
           :  |              | :: : |          || |:  | |    | :   |:
Db    1960 ERFPLSTPAFQGCMKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD 2019

Qy     209 VETLDTQHLRVDF-------TLWNESTPYQVLLESFSD 239
           | :||   |  | |       || |  |    || :  |
Db    2020 VPSLDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLED 2057
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RESULT  14
DP3A_VIBCH
ID   DP3A_VIBCH     STANDARD;      PRT;  1164 AA.
AC   P52022; Q9KPW7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-2000 (Rel. 40, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7).
GN   DNAE OR VC2245.
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EL TOR INABA C6706 / SEROTYPE O1;
RX   MEDLINE=97074686; PubMed=8917113;
RA   Franco A.A., Yeh P.E., Johnson J.A., Barry E.M., Guerra H., Maurer R.,
RA   Morris J.G. Jr.;
RT   "Cloning and characterization of dnaE, encoding the catalytic subunit
RT   of replicative DNA polymerase III, from Vibrio cholerae strain
RT   C6706.";
RL   Gene 175:281-283(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EL TOR N16961 / SEROTYPE O1;
RX   MEDLINE=20406833; PubMed=10952301;
RA   Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA   Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA   Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA   Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA   McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
RA   Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA   Fraser C.M.;
RT   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT   cholerae.";
RL   Nature 406:477-483(2000).
CC   -!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC       RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC       THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC       THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
CC       N PYROPHOSPHATE + DNA(N).
CC   -!- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND
CC       THETA CHAINS) THAT CAN REPAIR SHORT GAPS CREATED BY NUCLEASE
CC       IN DUPLEX DNA. FOR EFFICIENT REPLICATION OF THE LONG, SINGLE-
CC       STRANDED TEMPLATES, POL III REQUIRES THE AUXILIARY CHAINS BETA,
CC       GAMMA, AND DELTA (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U30472; AAC44578.1; ALT_INIT.
DR   EMBL; AE004296; AAF95389.1; -.
DR   TIGR; VC2245; -.
KW   Transferase; DNA-directed DNA polymerase; DNA replication.
FT   CONFLICT    348    348       I -> V (IN REF. 1).
FT   CONFLICT    485    487       ALQ -> ELK (IN REF. 1).
FT   CONFLICT    685    685       T -> P (IN REF. 1).
FT   CONFLICT   1000   1000       V -> A (IN REF. 1).
FT   CONFLICT   1030   1030       M -> L (IN REF. 1).
FT   CONFLICT   1103   1103       E -> G (IN REF. 1).
FT   CONFLICT   1117   1117       V -> A (IN REF. 1).
SQ   SEQUENCE   1164 AA;  130604 MW;  EDAFE70BB830F293 CRC64;
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  Query Match             4.8%;  Score 85.5;  DB 1;  Length 1164;
  Best Local Similarity   19.9%;  Pred. No. 21;
  Matches   61;  Conservative   44;  Mismatches   91;  Indels  111;  Gaps   15;

Qy      21 LLLNVLAPGRASPRLLDFPAPVCAQEGL--------SCRVK------------------ 53
           |:  | | |  :  | ||   :|   ||        :| ||
Db      32 LVKKVAAMGMPAMALTDF-TNLC---GLVKFYSTAHNCGVKPIIGADFTLQSEEFGDELT 87

Qy      54 NSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQ---HGELVPVLHVEWTLQTDASILYLE 110
             | |  : :  ||||          | :|      | :  ||:   | ::    :: |
Db      88 KLTLLAKNNVGYKNLT----------LLISKAYLRGHVQHQPVIDKAWLVEHAEGLIVLS 137

Qy     111 G---AELSVLQLNTNER---LCVKFQ--------FLSMLQHHRKRWRFSFSHFVVDPGQE 156
           |    |:    |  |::    |::|          :| :::  |     |: || :|  ::
Db     138 GGKSGEVGRALLKGNQQQVERCIEFYQTHFADHFYLELIRTGRAD-EESYLHFALDVAEQ 196

Qy     157 YEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQH 216
           |:: |              ::::|                          || |: :
Db     197 YDLPV------------VATNEVVF------------------------ITEESFEAHE 219

Qy     217 LRV----DFTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQE------EFHQRANV 266
           :||     :|| :   |     : :  ||   |     ::||   |       |  :| ||
Db     220 IRVAIHDGYTLEDPRRPKNYSPKQYLRSEAEMC-----ELFADIPEALANSVEIAKRCNV 274

Qy     267 TFTLSKF 273
           |  | ::
Db     275 TVRLGEY 281
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RESULT  15
DBL_HUMAN
ID   DBL_HUMAN      STANDARD;      PRT;   925 AA.
AC   P10911; P14919;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   PROTO-ONCOGENE DBL PRECURSOR [CONTAINS: MCF2].
GN   DBL OR MCF2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=89052660; PubMed=3056717;
RA   Ron D., Tronick S.R., Aaronson S.A., Eva A.;
RT   "Molecular cloning and characterization of the human dbl proto-
RT   oncogene: evidence that its overexpression is sufficient to transform
RT   NIH/3T3 cells.";
```

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RL   EMBO J. 7:2465-2473(1988).
RN   [2]
RP   REVISIONS.
RA   Ron D.;
RL   Submitted (JUN-1989) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 498-925 FROM N.A.
RX   MEDLINE=88176886; PubMed=3281159;
RA   Eva A., Vecchio G., Rao C.D., Tronick S.R., Aaronson S.A.;
RT   "The predicted DBL oncogene product defines a distinct class of
RT   transforming proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:2061-2065(1988).
RN   [4]
RP   SEQUENCE OF 398-925 FROM N.A.
RX   MEDLINE=94167115; PubMed=2577874;
RA   Noguchi T., Galland F., Batoz M., Mattei M.-G., Birnbaum D.;
RT   "Activation of a mcf.2 oncogene by deletion of amino-terminal coding
RT   sequences.";
RL   Oncogene 3:709-715(1988).
RN   [5]
RP   DBL-HOMOLOGY DOMAIN, AND MUTAGENESIS.
RX   MEDLINE=91291759; PubMed=2065022;
RA   Ron D., Zannini M., Lewis M., Wickner R.B., Hunt L.T., Graziani G.,
RA   Tronick S.R., Aaronson S.A., Eva A.;
RT   "A region of proto-dbl essential for its transforming activity shows
RT   sequence similarity to a yeast cell cycle gene, CDC24, and the human
RT   breakpoint cluster gene, bcr.";
RL   New Biol. 3:372-379(1991).
RN   [6]
RP   CHARACTERIZATION OF DBL DOMAIN.
RX   MEDLINE=94103281; PubMed=8276860;
RA   Hart M.J., Eva A., Zangrilli D., Aaronson S.A., Evans T.,
RA   Cerione R.A., Zheng Y.;
RT   "Cellular transformation and guanine nucleotide exchange activity are
RT   catalyzed by a common domain on the dbl oncogene product.";
RL   J. Biol. Chem. 269:62-65(1994).
CC   -!- FUNCTION: PROMOTES THE EXCHANGE OF G25K-BOUND GDP BY GTP. ACTS AS
CC       A GUANINE NUCLEOTIDE EXCHANGE FACTOR FOR CDC42 AND RHOA, BUT NOT
CC       FOR RAC1 AND TC10. CAN BE ACTIVATED BY TRUNCATION OF THE N-
CC       TERMINUS.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN AND ADRENAL GLANDS;
CC       IN THE ADULT, EXPRESSION IS LIMITED TO TESTES, OVARIES AND BRAIN.
CC   -!- DOMAIN: THE DH DOMAIN IS ESSENTIAL FOR TRANSFORMING ACTIVITY AND
CC       DIRECTLY CATALYZES GDP-GTP EXCHANGE ACTIVITY.
CC   -!- DISEASE: MCF.2 AND DBL REPRESENT TWO ACTIVATED VERSIONS OF THE
CC       SAME PROTO-ONCOGENE.
CC   -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
CC   -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X12556; CAA31069.1; -.
DR   EMBL; J03639; AAA52172.1; ALT_INIT.
DR   EMBL; X13230; CAA31617.1; ALT_SEQ.
DR   PIR; A30040; TVHUDB.
DR   PIR; A28051; TVHUBD.
DR   MIM; 311030; -.
DR   InterPro; IPR000219; -.
DR   InterPro; IPR000947; -.
DR   InterPro; IPR001331; -.
DR   InterPro; IPR001849; -.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   PRINTS; PR00615; CCAATSUBUNTA.
DR   PROSITE; PS00741; GDS_CDC24; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Guanine-nucleotide releasing factor; Proto-oncogene; Phosphorylation;
KW   Transforming protein.
FT   CHAIN       398    925       MCF2 TRANSFORMING PROTEIN.
FT   CHAIN       498    925       DBL TRANSFORMING PROTEIN.
FT   DOMAIN      498    686       DH.
FT   DOMAIN      687    809       PH.
FT   MOD_RES     742    742       PHOSPHORYLATION.
FT   MUTAGEN     640    646       LLLKELL->IIIRDII: TRANSFORMATION
FT                                CAPABILITY REDUCED; NO STIMULATION OF GDP
FT                                DISSOCIATON.
FT   CONFLICT    634    634       R -> Q (IN REF. 4).
FT   CONFLICT    886    886       A -> V (IN REF. 3).
SQ   SEQUENCE   925 AA;  107657 MW;  0BCCB303276D19C9 CRC64;


  Query Match             4.8%;  Score 85;  DB 1;  Length 925;
  Best Local Similarity   25.2%;  Pred. No. 18;
  Matches   33;  Conservative   22;  Mismatches   58;  Indels   18;  Gaps    4;

Qy     178 KIIFVPDCEDSKMKMTTSCVSSGSLWD---PNITVETLDTQHLRVDFTLWNESTPYQVLL 234
           ||  ||||:: :    :| : :|:  |    ::  | : |: : |          | |||
Db     467 KIEVVPDCQEKRSSGPSSSLDNGNSLDVLKNHVLNELIQTERVYV-------RELYTVLL 519

Qy     235 ESFSDSENHSCFDVV-------KQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFF 287
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Qy     288 SSCLNDCLRHA 298
             :|   :|
Db     579 LERKDDFQMYA 589


Search completed: July 17, 2001, 11:21:04
Job time: 158 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:16:31 ; Search time 21.86 Seconds
(without alignments)
296.733 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCWPRVVPGPALGWLL.....CPVISNTTVPKPVADYIPLW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1766	100.0	864	2	US-08-620-694A-2	Sequence 2, Appli
2	1766	100.0	864	3	US-09-022-255-2	Sequence 2, Appli
3	1766	100.0	864	3	US-09-022-696-2	Sequence 2, Appli
4	1766	100.0	864	3	US-08-978-773-2	Sequence 2, Appli
5	1766	100.0	864	3	US-09-022-253-2	Sequence 2, Appli
6	1766	100.0	864	3	US-09-022-260-2	Sequence 2, Appli
7	1766	100.0	864	4	US-09-022-259-2	Sequence 2, Appli
8	1766	100.0	864	4	US-09-022-257-2	Sequence 2, Appli
9	1254	71.0	866	2	US-08-620-694A-10	Sequence 10, Appl
10	1254	71.0	866	3	US-09-022-255-10	Sequence 10, Appl
11	1254	71.0	866	3	US-09-022-696-10	Sequence 10, Appl
12	1254	71.0	866	3	US-08-978-773-4	Sequence 4, Appli
13	1254	71.0	866	3	US-09-022-253-10	Sequence 10, Appl
14	1254	71.0	866	3	US-09-022-260-10	Sequence 10, Appl
15	1254	71.0	866	4	US-09-022-259-10	Sequence 10, Appl
16	1254	71.0	866	4	US-09-022-257-10	Sequence 10, Appl
17	97.5	5.5	379	4	US-08-908-436-5	Sequence 5, Appli
18	97	5.5	880	1	US-08-445-640-10	Sequence 10, Appl
19	97	5.5	880	3	US-08-170-558-10	Sequence 10, Appl
20	97	5.5	880	3	US-08-447-314-10	Sequence 10, Appl
21	97	5.5	880	3	US-08-445-461-10	Sequence 10, Appl
22	88	5.0	874	2	US-08-456-647B-6	Sequence 6, Appli
23	88	5.0	874	2	US-08-237-401A-6	Sequence 6, Appli
24	86.5	4.9	377	3	US-08-776-900C-2	Sequence 2, Appli
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26	86.5	4.9	377	4	US-08-225-487A-9	Sequence 9, Appli
27	86.5	4.9	377	4	US-09-268-195C-2	Sequence 2, Appli
28	86.5	4.9	377	5	PCT-US94-07127A-2	Sequence 2, Appli
29	86.5	4.9	377	5	PCT-US96-10521-12	Sequence 12, Appl
30	83.5	4.7	1213	1	US-08-188-582-20	Sequence 20, Appl
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44	81	4.6	2813	3	US-09-132-652-2	Sequence 2, Appli
45	79.5	4.5	364	1	US-08-680-726A-56	Sequence 56, Appl

ALIGNMENTS

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RESULT 1
US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 5869286el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694A
;      FILING DATE:  21 MARCH 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-620-694A-2
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  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     301 VPCPVISNTTVPKPVADYIPLW 322


RESULT   2
US-09-022-255-2
; Sequence 2, Application US/09022255
; Patent No. 6072033
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072033el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,255
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/620,694
;      FILING DATE:  21 MARCH 1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-255-2


  Query Match           100.0%;  Score 1766;  DB 3;  Length 864;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-183;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     301 VPCPVISNTTVPKPVADYIPLW 322
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RESULT   3
US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072037el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,696
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-696-2


  Query Match             100.0%;  Score 1766;  DB 3;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-183;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 2, Application US/08978773
; Patent No. 6083906
;  GENERAL INFORMATION:
;    APPLICANT:  Troutt, Anthony
;    TITLE OF INVENTION:  Method of Regulating Nitric Oxide Production
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple PowerMacintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for PowerMacintosh, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,773
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 60/052,525
;      FILING DATE:  27 NOVEMBER 1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2623-A
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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-773-2


  Query Match             100.0%;  Score 1766;  DB 3;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-183;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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US-09-022-253-2
; Sequence 2, Application US/09022253
; Patent No. 6096305
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6096305el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,253
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694
;      FILING DATE:  21-MARCH-1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-253-2


  Query Match             100.0%;  Score 1766;  DB 3;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-183;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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Db       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
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Db     301 VPCPVISNTTVPKPVADYIPLW 322


RESULT   6
US-09-022-260-2
; Sequence 2, Application US/09022260
; Patent No. 6100235
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6100235el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,260
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-260-2


  Query Match             100.0%;  Score 1766;  DB 3;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-183;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           ||||||||||||||||||||||
Db     301 VPCPVISNTTVPKPVADYIPLW 322


RESULT   7
US-09-022-259-2
; Sequence 2, Application US/09022259
; Patent No. 6191104
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6191104el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Apple Power Macintosh
;       OPERATING SYSTEM:  Apple Operating System 7.5.5
;       SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/022,259
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/620,694
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/410,535
;       FILING DATE:  23 MARCH 1995
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Perkins, Patricia Anne
;       REGISTRATION NUMBER:  34,695
;       REFERENCE/DOCKET NUMBER:  2617-B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206)587-0430
;       TELEFAX:  (206)
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;      LENGTH: 864 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-022-259-2


  Query Match           100.0%;  Score 1766;  DB 4;  Length 864;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-183;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
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Db     301 VPCPVISNTTVPKPVADYIPLW 322


RESULT   8
US-09-022-257-2
; Sequence 2, Application US/09022257
; Patent No. 6197525
;  GENERAL INFORMATION:
;     APPLICANT:  Yao, Zhengbin
;     APPLICANT:  Spriggs, Melanie
;     APPLICANT:  Fanslow, William
;     TITLE OF INVENTION:  No. 6197525el Receptor That Binds IL-17
;     NUMBER OF SEQUENCES:  10
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Immunex Corporation
;       STREET:  51 University Street
;       CITY:  Seattle
;       STATE:  WA
;       COUNTRY:  USA
;       ZIP:  98101
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Apple Power Macintosh
;       OPERATING SYSTEM:  Apple Operating System 7.5.5
;       SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/022,257
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/620,694
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/410,535
;       FILING DATE:  23 MARCH 1995
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Perkins, Patricia Anne
;       REGISTRATION NUMBER:  34,695
;       REFERENCE/DOCKET NUMBER:  2617-B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206)587-0430
;       TELEFAX:  (206)
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;      LENGTH: 864 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-022-257-2


  Query Match           100.0%;  Score 1766;  DB 4;  Length 864;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-183;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
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Db     301 VPCPVISNTTVPKPVADYIPLW 322


RESULT   9
US-08-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
;  GENERAL INFORMATION:
;     APPLICANT:  Yao, Zhengbin
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;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 5869286el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694A
;      FILING DATE:  21 MARCH 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-620-694A-10


  Query Match             71.0%;  Score 1254;  DB 2;  Length 866;
  Best Local Similarity   71.4%;  Pred. No. 7.3e-128;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           |||||:|||||||||:: | |  : || |:| || |:||||||||||||||||||||||||
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||:||
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||| ::||:|| |:|||||||||||||:   ||| |||||||| ||:|| ||
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||: :  | ||| ||||||:||| ||     || | ||:|||||||||||||: |
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           | || : :|  |:|: ||:|||
Db     301 VSCPEMPDT--PEPIPDYMPLW 320
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RESULT  10
US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072033el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,255
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/620,694
;      FILING DATE:  21 MARCH 1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-255-10


  Query Match             71.0%;  Score 1254;  DB 3;  Length 866;
  Best Local Similarity   71.4%;  Pred. No. 7.3e-128;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
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Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||:||
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
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Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
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Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
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Qy    301 VPCPVISNTTVPKPVADYIPLW 322
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Db    301 VSCPEMPDT--PEPIPDYMPLW 320


RESULT 11
US-09-022-696-10
; Sequence 10, Application US/09022696
; Patent No. 6072037
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072037el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,696
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-696-10


  Query Match           71.0%;  Score 1254;  DB 3;  Length 866;
  Best Local Similarity  71.4%;  Pred. No. 7.3e-128;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy      1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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Qy     61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
          |||||:|||||||:: | |  : || |:| || |:|||||||||||||||||||||||||
Db     61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy    121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
          |||||||:|:||| |:|| :||||:|||||||| |||||||||||||||||||:||
Db    121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy    181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
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Db    181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy    241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
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Db    241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy    301 VPCPVISNTTVPKPVADYIPLW 322
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Db    301 VSCPEMPDT--PEPIPDYMPLW 320


RESULT 12
US-08-978-773-4
; Sequence 4, Application US/08978773
; Patent No. 6083906
;  GENERAL INFORMATION:
;    APPLICANT:  Troutt, Anthony
;    TITLE OF INVENTION:  Method of Regulating Nitric Oxide Production
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple PowerMacintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for PowerMacintosh, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,773
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 60/052,525
;      FILING DATE:  27 NOVEMBER 1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2623-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-773-4


  Query Match           71.0%;  Score 1254;  DB 3;  Length 866;
  Best Local Similarity  71.4%;  Pred. No. 7.3e-128;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy      1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
          |   |  |  |||| || ||||| ||||| || |||| | ||:| ||:| |||||||||
Db      1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy     61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
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Db     61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy    121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
          |||||||:|:||| |:|| :||||:|||||||| |||||||||||||||||||:||
Db    121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy    181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
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Db    181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy    241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
          ||||||: :  | ||| ||||||:||| ||     || | ||:|||||||||||||: |
Db    241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy    301 VPCPVISNTTVPKPVADYIPLW 322
          | || : :|  |:|: ||:|||
Db    301 VSCPEMPDT--PEPIPDYMPLW 320


RESULT 13
US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6096305el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,253
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694
;      FILING DATE:  21-MARCH-1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-253-10


  Query Match           71.0%;  Score 1254;  DB 3;  Length 866;
  Best Local Similarity  71.4%;  Pred. No. 7.3e-128;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy      1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
          |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db      1 MGAARSPPSAVPGPLLLGLLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy     61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
          |||||:||||||:: | |  : || |:| || |:||||||||||||||||||||||||
Db     61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy    121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
          |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||:||
Db    121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy    181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||| ::||:|| |:|||||||||||||:   ||| |||||||| ||:|| ||
Db    181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy    241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
          ||||||: :  | ||| ||||||:||| ||     || | ||:|||||||||||||: |
Db    241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy    301 VPCPVISNTTVPKPVADYIPLW 322
          | || : :|  |:|: ||:|||
Db    301 VSCPEMPDT--PEPIPDYMPLW 320


RESULT 14
US-09-022-260-10
; Sequence 10, Application US/09022260
; Patent No. 6100235
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6100235el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,260
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-260-10


  Query Match           71.0%;  Score 1254;  DB 3;  Length 866;
  Best Local Similarity  71.4%;  Pred. No. 7.3e-128;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;
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Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           |||||:|||||||:: | |  : || |:| || |:|||||||||||||||||||||||||
Db      61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||:||
Db     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
            ||||| ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||: :  | ||| ||||||:||| ||     || | ||:|||||||||||||: |
Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           | || : :|  |:|: ||:|||
Db     301 VSCPEMPDT--PEPIPDYMPLW 320


RESULT  15
US-09-022-259-10
; Sequence 10, Application US/09022259
; Patent No. 6191104
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6191104el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,259
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-09-022-259-10

Query Match 71.0%; Score 1254; DB 4; Length 866;
Best Local Similarity 71.4%; Pred. No. 7.3e-128;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

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Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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Db       1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
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Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
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Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
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Db     241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
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Db     301 VSCPEMPDT--PEPIPDYMPLW 320
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Search completed: July 17, 2001, 11:19:22
Job time: 171 sec

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:17:26 ; Search time 26.59 Seconds
(without alignments)
922.460 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCWPRVVPGPALGWLL.....CPVISNTTVPKPVADYIPLW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	113	6.4	2311	1	TVCHSR	kinase-related pro
2	112.5	6.4	708	2	T50064	probable transcrip
3	101	5.7	880	1	JC4166	protein-tyrosine k
4	99.5	5.6	1506	2	T30886	integumentary muci
5	99	5.6	449	2	A36303	gamma-aminobutyric
6	99	5.6	449	2	I52630	GABAA receptor del
7	98	5.5	1748	2	S63127	probable membrane
8	97	5.5	880	2	B53743	protein-tyrosine k
9	95	5.4	449	2	A34625	gamma-aminobutyric
10	94	5.3	388	2	A45304	granulocyte/macrop
11	92	5.2	682	2	G86300	hypothetical prote
12	91.5	5.2	3131	2	T39553	vacuolar protein s
13	91	5.2	333	2	T26891	hypothetical prote
14	89.5	5.1	606	2	T08180	PF20 protein, micr
15	89.5	5.1	885	2	S42841	T16G12.1 protein -
16	88.5	5.0	308	2	C30554	Ig heavy chain C r
17	88.5	5.0	472	2	S31459	Ig gamma-1 chain -
18	88.5	5.0	954	2	S46105	glucan 1,4-alpha-g
19	88	5.0	1231	2	S53089	protein-tyrosine-p
20	88	5.0	1323	2	T37533	coronin-like prote
21	87.5	5.0	416	2	T10623	hypothetical prote
22	87.5	5.0	577	2	I50731	Ig heavy chain - n
23	87.5	5.0	1188	2	T13933	pol polyprotein -
24	87	4.9	520	2	S45702	leukotriene-B4 20-
25	87	4.9	2515	2	A41519	posterior-group pr
26	86.5	4.9	377	2	A57511	interleukin-1 beta
27	85.5	4.8	1164	2	G82100	DNA polymerase III
28	85	4.8	567	2	S10138	mcf2 protein - hum
29	85	4.8	925	1	TVHUDB	transforming prote
30	84.5	4.8	429	1	EHRT	Ig epsilon chain C
31	84.5	4.8	712	2	T02312	hypothetical prote
32	84.5	4.8	1747	1	A45974	collagen alpha 1(X
33	84	4.8	243	2	S25755	Ig lambda chain -
34	83.5	4.7	304	2	B83541	probable polynucle
35	83.5	4.7	1213	2	A54063	TATA-binding prote
36	83	4.7	432	1	A41056	brachyury homolog
37	83	4.7	672	1	KIHUCA	protein kinase C (
38	83	4.7	672	1	KIRTC	protein kinase C (
39	83	4.7	672	1	KIMSCA	protein kinase C (
40	83	4.7	672	1	KIRBC	protein kinase C (
41	83	4.7	1038	2	S06046	integrin alpha-4 c
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43	82.5	4.7	318	2	S52424	homeodomain protei
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45	82.5	4.7	399	2	T41786	P47 orf40 - Bombyx

ALIGNMENTS

RESULT 1
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kinase-related protein ros precursor - chicken
N;Alternate names: sevenless homolog c-ros
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) ros
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1989 #sequence_revision 07-Oct-1994 #text_change 16-Jun-2000
C;Accession: A60197; A28357; A25225
R;Chen, J.; Heller, D.; Poon, B.; Kang, L.; Wang, L.H.
Oncogene 6, 257-264, 1991
A;Title: The proto-oncogene c-ros codes for a transmembrane tyrosine protein kinase s
A;Reference number: A60197; MUID:91156299
A;Accession: A60197
A;Molecule type: mRNA
A;Residues: 1-2311 <CHE>
A;Note: authors translated the codon GGA for residue 961 as Ser, AAT for residue 962
R;Podell, S.B.; Sefton, B.M.
Oncogene 2, 9-14, 1987
A;Title: Chicken proto-oncogene c-ros cDNA clones: identification of a c-ros RNA tran
A;Reference number: A28357; MUID:88143715
A;Accession: A28357
A;Molecule type: mRNA
A;Residues: 2010-2139,'LP',2142-2311 <POD>
A;Cross-references: GB:X06770; NID:g63775; PIDN:CAA29938.1; PID:g1334743
R;Neckameyer, W.S.; Shibuya, M.; Hsu, M.T.; Wang, L.H.
Mol. Cell. Biol. 6, 1478-1486, 1986
A;Title: Proto-oncogene c-ros codes for a molecule with structural features common to
A;Reference number: A25225; MUID:87064428
A;Accession: A25225
A;Molecule type: DNA
A;Residues: 1868-2139,'LP',2142-2254,'SSTKLLRVSLGSAVPTAFAQTCNSVNVESQNGLGWKGP' <NEC>
A;Cross-references: GB:M13013; NID:g212636; PIDN:AAA49058.1; PID:g212637
C;Genetics:
A;Gene: ros
C;Superfamily: kinase-related protein ros; LDL receptor YWTD-containing repeat homolo
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas
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F;28-2311/Product: kinase-related protein ros #status predicted <MAT>
F;28-1873/Domain: extracellular #status predicted <EXT>
F;344-387/Domain: LDL receptor YWTD-containing repeat homology <YW1>
F;475-512/Domain: LDL receptor YWTD-containing repeat homology <YW2>
F;715-758/Domain: LDL receptor YWTD-containing repeat homology <YW3>
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F;800-839/Domain: LDL receptor YWTD-containing repeat homology <YW5>
F;844-889/Domain: LDL receptor YWTD-containing repeat homology <YW6>
F;894-934/Domain: LDL receptor YWTD-containing repeat homology <YW7>
F;1546-1587/Domain: LDL receptor YWTD-containing repeat homology <YW7>
F;1874-1899/Domain: transmembrane #status predicted <TMN>
F;1900-2311/Domain: intracellular #status predicted <INT>
F;1959-2239/Domain: protein kinase homology <KIN>
F;1967-1975/Region: protein kinase ATP-binding motif
F;49,65,77,123,132,265,287,307,333,377,480,607,628,706,714,911,940,962,971,1110,1154,

```
ent) #status predicted
F;1996/Active site: Lys #status predicted
F;2127,2131,2132/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat

  Query Match             6.4%;  Score 113;  DB 1;  Length 2311;
  Best Local Similarity   20.5%;  Pred. No. 0.77;
  Matches   62;  Conservative   45;  Mismatches  127;  Indels   68;  Gaps   12;

Qy      70 PSSPKNIYINLSVSSTQHGELVPVLHVEW----------TLQTDASILYLEGAELSVLQ 118
           ||:| |  | :  |:|  ||   :: : |          :   :||  ||  :::: 
Db    1049 PSAPANPRIYVLHSNTHEGEEKVLVELRWDKPERDNGVLTQFRVYYQLLYESGAADTLME 1108

Qy     119 LNTNERLCVKFQFLSMLQHHRKRWRFSFSHFV-VDPGQEYEVTVHH----LPKP------ 167
           | ::       |    :| |   ||    |  | ||   :|   :     | |
Db    1109 WNVSDVKPTALLFSIRDEHPRLTVRFQVQAFTSVGPGPMSDVAQRNSSDIFPVPTLITFS 1168

Qy     168 -----IPDGDPNH------------------KSKIIFVPDCEDSKMKMTTSCVSSGSLW 203
                : | | ||                    |: ::   |||   :     |   |:
Db    1169 SNKLFLTDIDSNHTIWEVLTNRNIKDICYTADDDKVYYI--LEDSLFLLNVQSTSESQLF 1226

Qy     204 DP----NITVETLD--TQHLRVDF-TLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPR 256
           :     |:|  |:|   :|| |   | |||:  : : ||  : |       :      |
Db    1227 EDVFLRNVTAITVDWIARHLFVAMKTSWNETQVFFIDLELKTKS-----LKALNIQLGKR 1281

Qy     257 QEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPKPVA 316
                :  | ||: :|        : |:   ||: : |       ::   :| : :
Db    1282 NSTISSLLSYPF-LSRLYWIEELDYGSRMFYYDILNNTMYH-------ILGYESVEEKMR 1333

Qy     317 DY 318
           :|
Db    1334 NY 1335


RESULT   2
T50064
probable transcription activator [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50064
R;Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z25032
A;Accession: T50064
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-708 <HAR>
A;Cross-references: EMBL:AL157994; PIDN:CAB76236.1; GSPDB:GN00066; SPDB:SPAC105.03c
A;Experimental source: strain 972h(-); cosmid c105
C;Genetics:
A;Gene: SPDB:SPAC105.03c
A;Map position: 1

  Query Match             6.4%;  Score 112.5;  DB 2;  Length 708;
  Best Local Similarity   21.6%;  Pred. No. 0.19;
  Matches   63;  Conservative   45;  Mismatches   78;  Indels  105;  Gaps   15;

Qy      44 AQEGLSCRVKNSTCL-------DDSWIHPKNLTPSSPKNIYINL--------------SV 82
           ||  |        |||          |:: | :|  |||   | ||                ||
Db      14 AQPNLCIPCSLGTCLIHFHEFSSSSFMDPVSLFCSSP---YPNLPPHSRSSSLESKKPSV 70

Qy      83 SS------------TQHGELVPVLHVE---WTLQTDASILYLEGAELSVLQLNTNERLCV 127
           :|            | :  |:|     |   ||:: ::    | |:     :|
Db      71 ASQDVKSDGTLPIGTNNNPLIPSHSQESSHWTIRHESMPSALAGSSAQSMQ--------- 121

Qy     128 KFQFLSMLQHHRK-RWRFSFSHFVVDPGQEYEVTVHHLPKPI------PDGDPNHKSKII 180
             || |: |:    |:: ||:                  |:||     |  :|  :   :
Db     122 --QFPSITQNEENFRFKKSFTQ---------------PQPIVKETTFPPKSEPGQEHAKL 163

Qy     181 -------FVPDCEDSKMKMTT------SCVSSGSLWDPNITV----ETLDTQHLRVDFTL 223
                  |:     :|::  :       | ::| :: | | ::      ::| |    ||
Db     164 SDLSYEEFLKKYSSTKVERVSEAAPPPSSLNSSTVLDENDSLISQGSSVDDQ---TDFLG 220

Qy     224 WNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFH 274
           :::|  |  :|   |||:     |:::| | |::          |:| |  |
Db     221 FDDSLSYAYILNPTSDSD----VDLIRQYFIPKEG--------TYTFSNMH 259


RESULT   3
JC4166
protein-tyrosine kinase (EC 2.7.1.112) tyro3 precursor - rat
N;Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JC4166; PT0185
R;Ohashi, K.; Honda, S.; Ichinomiya, N.; Nakamura, T.; Mizuno, K.
J. Biochem. 117, 1267-1275, 1995
A;Title: Molecular cloning and in situ localization in the brain of rat Sky receptor
A;Reference number: JC4166; MUID:96104999
A;Accession: JC4166
A;Molecule type: mRNA
A;Residues: 1-880 <OHA>
A;Cross-references: DDBJ:D37880; NID:g1498195; PIDN:BAA07119.1; PID:g829057
A;Experimental source: brain
A;Note: It is uncertain whether Met-1 or Met-7 is the initiator
R;Lai, C.; Lemke, G.
Neuron 6, 691-704, 1991
A;Title: An extended family of protein-tyrosine kinase genes differentially expressed
A;Reference number: PT0183; MUID:91222560
A;Accession: PT0185
A;Molecule type: mRNA
A;Residues: 650-703 <LAI>
A;Experimental source: sciatic nerve
C;Comment: This receptor plays an important role in development, function, and mainte
C;Genetics:
A;Gene: tyro-3
C;Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; imm
C;Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transformi
F;1-31/Domain: (or 7-31) signal sequence #status predicted <SIG>
F;32-880/Product: (or 32-874) protein-tyrosine kinase tyro3 #status predicted <MAT>
F;50-109/Domain: immunoglobulin homology <IMM1>
F;146-195/Domain: immunoglobulin homology <IMM2>
F;214-299/Domain: fibronectin type III repeat homology <FN3A>
F;312-395/Domain: fibronectin type III repeat homology <FN3B>
F;419-441/Domain: transmembrane #status predicted <TMM>
F;506-783/Domain: protein kinase homology <KIN>
F;514-522/Region: protein kinase ATP-binding motif
F;515-766/Domain: cytoplasmic tyrosine kinase #status predicted <CTK>
F;53,75,181,220,230,283,356,370/Binding site: carbohydrate (Asn) (covalent) #status p

  Query Match             5.7%;  Score 101;  DB 1;  Length 880;
  Best Local Similarity   21.4%;  Pred. No. 2.2;
  Matches   78;  Conservative   53;  Mismatches  129;  Indels  104;  Gaps   19;

Qy       1 MAIRRCWPRVVPGPALGWLLL--LLNVLAPGRASP--RLLDFPAPVCAQEG----LSCRV 52
           ||:||   |    | |  |||  | ::| || |:   :|:  |  :   :|    |:| |
Db       1 MALRRSMGR----PGLRPLLLAGLASLLLPGSAAAGLKLMGAPVKMTVSQGQPVKLNCSV 56

Qy      53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGA 112
           :     |  |:    :  :: :   :::|:|       : :| ::   ::|| : : :
Db      57 EGMDDPDIHWMKDGAVVQNASQ---VSISISEQ---NWIGLLSLKSAERSDAGLYWCQVK 110

Qy     113 ELSVLQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDP-----------------G 154
           :    ::: :  | |:                        | |:|               |
Db     111 DGEETKISQSVWLTVE---------------GVPFFTVEPKDLAVPPNVPFQLSCEAVG 154

Qy     155 QEYEVTVHHLPKPIPDGDPNHKSKIIFVP--------DCEDSKMK-MTTSCVSSGSLWDP 205
           ||:     |   | |      :: |              ||   :| : ||  :    |  |
Db     155 PPEPVTIFWWRGPTKVGGPASSPSVLNVTGVTQRTEFSCEAHNIKGLATSRPAIIRLQAP 214

Qy     206 -----NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQEEF 260
                |||| |: : :  |    |         ||        |||   |:   ||   |:
Db     215 PAAPFNITVTTISSSNASV---AWVPGADGLALL--------HSC--TVQVAHAP--GEW 259
```

```
Qy    261 HQRANVTFTLSKFHWCCHHHVQVQPFFSSC----LNDCLRHAVTVPCPVISNTTVPKPVA 316
Db    260 EALAVV-------------VPVPPF--TCLLRNLAPATNYSLRVRC---ANALGPSPYG 300

Qy    317 DYIP 320
Db    301 DWVP 304
```

RESULT 4
T30886
integumentary mucin B.1 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000
C;Accession: T30886
R;Joba, W.; Hoffmann, W.
J. Biol. Chem. 272, 1805-1810, 1997
A;Title: Similarities of integumentary mucin B.1 (FIM-B.1) from Xenopus laevis and prepr
A;Reference number: Z20920; MUID:97153143
A;Accession: T30886
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1506 <JOB>
A;Cross-references: EMBL:Y08296; NID:g1839051; PIDN:CAA69604.1; PID:g1839052
C;Genetics:
A;Note: FIM-B.1
C;Superfamily: pig submaxillary mucin

Query Match 5.6%; Score 99.5; DB 2; Length 1506;
Best Local Similarity 21.1%; Pred. No. 5.9;
Matches 63; Conservative 35; Mismatches 110; Indels 91; Gaps 16;

```
Qy     56 TCLDDSWIHPKNLTPSSPK---NIYINL--SVSSTQHGELVPV--LHVEW---------- 98
Db    495 TCNGGTWTCSKGSCPGICKVEEGVYVTTYDGITYSMHGNCVYIISMHTSWLVYAKLSQSQ 554

Qy     99 -----TLQTDASILYLEGAELSVLQLN----------TNERLCVKFQ--------FLSML 135
Db    555 DAQSSTIINSVSLVLNLGNQESTYTFNRDGSIINEKMTNQNVFQSDQLSISRSGTFIIVL 614

Qy    136 QHHRKRWRF----SFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMK 191
Db    615 THLHVNLLIQTGTTMQFYTSVPSTGYEDTEG------PCGSFNHKADDDFM-----SNQK 663

Qy    192 MTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQ 251
Db    664 M------------PESSPETF------VGF--WK--------MSSCSDPVKPTCIDLEKE 695

Qy    252 IFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLN-DCLRHAVTVP-CPVISN 308
Db    696 LFANQQCSQLKDPNGAFAK------CHSTVLYRSFYERCVHLTCISQDMTVSMCTELRN 748
```

RESULT 5
A36303
gamma-aminobutyric acid receptor A delta chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Aug-1999
C;Accession: A36303
R;Sommer, B.; Poustka, A.; Spurr, N.K.; Seeburg, P.H.
DNA Cell Biol. 9, 561-568, 1990
A;Title: The murine GABA-A receptor delta-subunit gene: structure and assignment to huma
A;Reference number: A36303; MUID:91103876
A;Accession: A36303
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-449 <SOM>
A;Cross-references: GB:M60587; GB:M60588; GB:M60589; GB:M60591; GB:M60592; GB:M60593; GE
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

Query Match 5.6%; Score 99; DB 2; Length 449;
Best Local Similarity 22.5%; Pred. No. 1.4;
Matches 64; Conservative 44; Mismatches 84; Indels 92; Gaps 17;

```
Qy     16 LGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKN------STCLDDSWI------ 63
Db      4 LGWLLL-----------PLLL-----LCTQPHHGARAMNDIGDYVGSNLEISWLPNLDGL 47

Qy     64 ---HPKNLTP---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL 117
Db     48 MEGYARNFRPGIGGAPVNVALALEVASIDH---ISEANMEYTMTV---FLHQSWRDSRLS 101

Qy    118 QLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQE--YEVTVHH-LPKPIPDGDPN 174
Db    102 YNHTNETLGLDSRFVDKL--------WLPDTFIVNAKSAWFHDVTVENKLIRLQPDG--- 150

Qy    175 HKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLL 234
Db    151 ---VILY-----SIRITSTVAC-------DMDLAKYPLDEQECMLD-------------L 182

Qy    235 ESFSDSENHSCFDVVKQIFAPRQEEFH-----QRANVTFTLSKF 273
Db    183 ESY----GYSSEDIV-YYWSENQEQIHGLDRLQLAQFTITSYRF 221
```

RESULT 6
I52630
GABAA receptor delta subunit - mouse
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C;Accession: I52630
R;Wang, J.B.; Kofuji, P.; Burt, D.R.
Brain Res. Bull. 29, 119-123, 1992
A;Title: Strain comparisons and developmental profile of the delta subunit of the mur
A;Reference number: I52630; MUID:92370453
A;Accession: I52630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-449 <RES>
A;Cross-references: GB:S42882; NID:g253879; PIDN:AAB22967.1; PID:g253880
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match 5.6%; Score 99; DB 2; Length 449;
Best Local Similarity 22.5%; Pred. No. 1.4;
Matches 64; Conservative 44; Mismatches 84; Indels 92; Gaps 17;

```
Qy     16 LGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKN------STCLDDSWI------ 63
Db      4 LGWLLL-----------PLLL-----LCTQPHHGARAMNDIGDYVGSNLEISWLPNLDGL 47

Qy     64 ---HPKNLTP---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL 117
Db     48 MEGYARNFRPGIGGAPVNVALALEVASIDH---ISEANMEYTMTV---FLHQSWRDSRLS 101

Qy    118 QLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQE--YEVTVHH-LPKPIPDGDPN 174
Db    102 YNHTNETLGLDSRFVDKL--------WLPDTFIVNAKSAWFHDVTVENKLIRLQPDG--- 150

Qy    175 HKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLL 234
Db    151 ---VILY-----SIRITSTVAC-------DMDLAKYPLDEQECMLD-------------L 182

Qy    235 ESFSDSENHSCFDVVKQIFAPRQEEFH-----QRANVTFTLSKF 273
Db    183 ESY----GYSSEDIV-YYWSENQEQIHGLDRLQLAQFTITSYRF 221
```

RESULT 7
S63127
probable membrane protein YNL172w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N1677

```
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 06-Feb-1998
C;Accession: S63127
R;Obermaier, B.; Piravandi, E.; Rinke, M.; Domdey, H.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63122
A;Accession: S63127
A;Molecule type: DNA
A;Residues: 1-1748 <OBE>
A;Cross-references: EMBL:Z71448; NID:g1302143; PID:e239542; PID:g1302144; MIPS:YNL172w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:APC1
A;Cross-references: SGD:S0005116; MIPS:YNL172w
A;Map position: 14L
C;Keywords: transmembrane protein
F;578-594/Domain: transmembrane #status predicted <TM1>
F;1247-1263/Domain: transmembrane #status predicted <TM2>
F;1382-1398/Domain: transmembrane #status predicted <TM3>


  Query Match             5.5%;  Score 98;  DB 2;  Length 1748;
  Best Local Similarity   22.9%;  Pred. No. 9.4;
  Matches   69;  Conservative   38;  Mismatches  104;  Indels   90;  Gaps   16;

Qy      29 GRASPRLLDFPAP-VCAQEGLSC---RVKNSTCLDDSWIHPKNLTPSSPKNIYINLSVSS 84
           | || |   |  |  |::  ||    |: |:       | | |   ::|   : : | ::
Db     289 GNASGRTDIFALPSSCSRRSLSATLDRMGNN-------IAPTN--RAAPSGFFDSSSANT 339

Qy      85 TQHGELVPV------LHVEWTLQTDASILYLEGAELSVLQLN-----TNERL---CVKFQ 130
             |  : ||         |:  ||  |   :   |:| |:|      |: ||     | :
Db     340 ATHSNITPVSQPMQQQQQEYLNQTATSSKDIVLTEISSLKLPDDIIFTSRRLSSILSKLK 399

Qy     131 FLSML------------QHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKS 177
           |||:               |  | |       |:|           :|  |    | :
Db     400 FLSLRFERREGLLIFHEPTHFCKIWLIDLLPDVLD----------SIPFKIYGNSPQNMI 449

Qy     178 KIIFVPDCEDSKMK-----------MTTSC---VSSGS--------LWDPNITVETLDT 214
           ::      |: |:|             :  ||   || |         |:|| : : |  :
Db     450 RL------ENLKLKEPSRIQAMYIHELLESCLILVSEGQNKEEYKACLYDPFVKI-TSPS 502

Qy     215 QHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFH 274
           :::  : |  |      | |      |    ||: || | :|         |::|    |
Db     503 KNISEELTKQNSLPSLQKLFPYPETSFTKLCFEAVKYITSP-------AFNISFI---FL 552

Qy     275 W 275
           |
Db     553 W 553


RESULT   8
B53743
protein-tyrosine kinase (EC 2.7.1.112) tyro3 precursor - mouse
N;Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse; tyros
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
C;Accession: B53743; S44141; JC2146; I49198; I49151; I48863; I48860
R;Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.
J. Biol. Chem. 269, 10720-10728, 1994
A;Title: rse, a novel receptor-type tyrosine kinase with homology to Axl/Ufo, is express
A;Reference number: A53743; MUID:94193774
A;Accession: B53743
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-880 <MAR>
A;Cross-references: GB:U05683; NID:g469518; PIDN:AAA19237.1; PID:g469519
R;Lai, C.; Gore, M.; Lemke, G.
submitted to the EMBL Data Library, March 1994
A;Description: Structure, expression and activity of TYRO3.
A;Reference number: S44141
A;Accession: S44141
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-629,'R',631-810,'V',812-880 <LAI>
A;Cross-references: EMBL:X78103; NID:g473096; PIDN:CAA54995.1; PID:g473097
R;Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Spritz, R.A.; Guida, L.C
Gene 134, 289-293, 1993
A;Title: The human TYRO3 gene and pseudogene are located in chromosome 15q14-q25.
A;Reference number: JC2145; MUID:94085793
A;Accession: JC2146
A;Molecule type: mRNA
A;Residues: 509-629,'R',631-647,'P',649-780 <POL>
R;Crosier, P.S.; Lewis, P.M.; Hall, L.R.; Vitas, M.R.; Morris, C.M.; Beier, D.R.; Woo
Growth Factors 11, 125-136, 1994
A;Title: Isolation of a receptor tyrosine kinase (DTK) from embryonic stem cells: str
A;Reference number: I49198; MUID:95161079
A;Accession: I49198
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-880 <RES>
A;Cross-references: EMBL:U18933; NID:g622982; PIDN:AAC52148.1; PID:g622983
R;Schulz, N.T.; Paulhiac, C.I.; Lee, L.; Zhou, R.
Brain Res. Mol. Brain Res. 28, 273-280, 1995
A;Title: Isolation and expression analysis of tyro3, a murine growth factor receptor
A;Reference number: I49151; MUID:95240399
A;Accession: I49151
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 7-880 <RE2>
A;Cross-references: EMBL:U18342; NID:g687625; PIDN:AAB26942.1; PID:g687626
R;Biesecker, L.G.; Giannola, D.M.; Emerson, S.G.
Oncogene 10, 2239-2242, 1995
A;Title: Identification of alternative exons, including a novel exon, in the tyrosine
A;Reference number: I48861; MUID:95303487
A;Accession: I48863
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-92 <RE3>
A;Cross-references: EMBL:U23721; NID:g901992; PIDN:AAC52217.1; PID:g901996
R;Lai, C.; Gore, M.; Lemke, G.
Oncogene 9, 2567-2578, 1994
A;Title: Structure, expression, and activity of Tyro 3, a neural adhesion-related rec
A;Reference number: I48860; MUID:94336210
A;Accession: I48860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 7-629,'R',631-810,'V',812-880 <RE4>
A;Cross-references: EMBL:X78103; NID:g473096; PIDN:CAA54995.1; PID:g473097
C;Genetics:
A;Gene: tyro3; Dtk; Etk2/tyro3
A;Introns: 32/1
C;Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; imm
C;Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transformi
F;1-31/Domain: (or 7-31) signal sequence #status predicted <SIG>
F;32-880/Product: protein-tyrosine kinase tyro3 #status predicted <MAT>
F;50-109/Domain: immunoglobulin homology <IMM1>
F;146-195/Domain: immunoglobulin homology <IMM2>
F;214-299/Domain: fibronectin type III repeat homology <FN3A>
F;312-395/Domain: fibronectin type III repeat homology <FN3B>
F;419-441/Domain: transmembrane #status predicted <TMM>
F;506-783/Domain: protein kinase homology <KIN>
F;514-522/Region: protein kinase ATP-binding motif
F;515-766/Domain: cytoplasmic tyrosine kinase #status predicted <CTK>
F;53,75,181,220,230,283,356,370/Binding site: carbohydrate (Asn) (covalent) #status p


  Query Match             5.5%;  Score 97;  DB 2;  Length 880;
  Best Local Similarity   21.0%;  Pred. No. 4.8;
  Matches   77;  Conservative   55;  Mismatches  126;  Indels  108;  Gaps   20;

Qy       1 MAIRRC--WPRVVPGPALGWLLL--LLNVLAPGRASP--RLLDFPAPVCAQEG----LSC 50
             ||:||   || : |      |||  | ::| || |:   :|:  |  :   :|    |:|
Db       1 MALRRSMGWPGLRP------LLLAGLASLLLPGSAAAGLKLMGAPVKMTVSQGQPVKLNC 54

Qy      51 RVKNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLE 110
             |:     |  |:    :  :: :     :|:| ::|   : :| ::   ::|| : : :
```

```
Db      55 SVEGMEDPDIHWMKDGTVVQNASQ-----VSISISEH-SWIGLLSLKSVERSDAGLYWCQ 108

Qy     111 GAELSVLQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDP----------------- 153

Db     109 VKDGEETKISQSVWLTVE---------------GVPFFTVEPKDLAVPPNAPFQLSCEA 152

Qy     154 -GQEYEVTVHHLPKPIPDGDPNHKSKIIFVP--------DCEDSKMK-MTTSCVSSGSLW 203

Db     153 VGPPEPVTIYWWRGLTKVGGPAPSPSVLNVTGVTQRTEFSCEARNIKGLATSRPAIVRLQ 212

Qy     204 DP-----NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQE 258

Db     213 APPAAPFNTTVTTISSYNASV---AWVPGADGLALL--------HSC--TVQVAHAP--G 257

Qy     259 EFHQRANVTFTLSKFHWCCHHHVQVQPFFSSC----LNDCLRHAVTVPCPVISNTTVPKP 314

Db     258 EWEALAVV--------------VPVPPF--TCLLRNLAPATNYSLRVRC---ANALGPSP 298

Qy     315 VADYIP 320

Db     299 YGDWVP 304
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RESULT 9
A34625
gamma-aminobutyric acid/benzodiazepine receptor type A delta chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34625; A53811; JQ0076
R;Zhao, Z.Y.; Joho, R.H.
Biochem. Biophys. Res. Commun. 167, 174-182, 1990
A;Title: Isolation of distantly related members in a multigene family using the polymera
A;Reference number: A34625; MUID:90179746
A;Accession: A34625
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-449 <ZHA>
A;Cross-references: GB:M35162; NID:g204207; PIDN:AAA41182.1; PID:g204208
R;Motejlek, K.; Haeuselmann, R.; Leitgeb, S.; Luescher, B.
J. Biol. Chem. 269, 15265-15273, 1994
A;Title: BSF1, a novel brain-specific DNA-binding protein recognizing a tandemly repeate
A;Reference number: A53811; MUID:94253091
A;Accession: A53811
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-26 <MOT>
A;Cross-references: GB:X69986
R;Shivers, B.D.; Killisch, I.; Sprengel, R.; Sontheimer, H.; Koehler, M.; Schofield, P.R
Neuron 3, 327-337, 1989
A;Title: Two novel GABA-A receptor subunits exist in distinct neuronal subpopulations.
A;Reference number: JQ0076; MUID:90380375
A;Accession: JQ0076
A;Molecule type: mRNA
A;Residues: 1-92,'RA',95-130,'VCLV',135-403,'VP',406-449 <SHI>
A;Experimental source: brain
C;Comment: Neurotransmission effected by gamma-aminobutyric acid (GABA) is mediated main
C;Comment: The GABA-A receptor consists of subunits that are structurally related to lig
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-449/Product: gamma-aminobutyric acid A receptor delta chain #status predicted <MAT>
F;249-271/Domain: transmembrane #status predicted <TM1>
F;275-297/Domain: transmembrane #status predicted <TM2>
F;309-331/Domain: transmembrane #status predicted <TM3>
F;427-449/Domain: transmembrane #status predicted <TM4>
F;103,106/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;164-178/Disulfide bonds: #status predicted

Query Match 5.4%; Score 95; DB 2; Length 449;
Best Local Similarity 22.2%; Pred. No. 3;
Matches 63; Conservative 44; Mismatches 85; Indels 92; Gaps 17;

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Qy      16 LGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKN------STCLDDSWI------ 63

Db       4 LGWLLL-----------PLLL-----LCTQPHHGARAMNDIGDYVGSNLEISWLPNLDGL 47

Qy      64 ---HPKNLTP---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL 117

Db      48 MEGYARNFRPGIGGPPVNVALALEVASIDH---ISEANMEYTMTV---FLHQSWRDSRLS 101

Qy     118 QLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQE--YEVTVHH-LPKPIPDGDPN 174

Db     102 YNHTNETLGLDSRFVDKL--------WLPDTFIVNAKSAWFHDVTVENKLIRLQPDG--- 150

Qy     175 HKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLL 234

Db     151 ---VILY-----SIRITSTVAC-------DMDLAKYPMDEQECMLD------------L 182

Qy     235 ESFSDSENHSCFDVVKQIFAPRQEEFH-----QRANVTFTLSKF 273

Db     183 ESY----GYSSEDIV-YYWSENQEQIHGLDRLQLAQFTITSYRF 221
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RESULT 10
A45304
granulocyte/macrophage colony-stimulating factor receptor, low affinity, precursor - :
C;Species: Mus musculus (house mouse)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C;Accession: A45304
R;Park, L.S.; Martin, U.; Sorensen, R.; Luhr, S.; Morrissey, P.J.; Cosman, D.; Larsen
Proc. Natl. Acad. Sci. U.S.A. 89, 4295-4299, 1992
A;Title: Cloning of the low-affinity murine granulocyte-macrophage colony-stimulating
A;Reference number: A45304; MUID:92262426
A;Accession: A45304
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-388 <PAR>
A;Cross-references: GB:M85078; NID:g192594; PIDN:AAA37421.1; PID:g192595
C;Keywords: transmembrane protein

Query Match 5.3%; Score 94; DB 2; Length 388;
Best Local Similarity 21.6%; Pred. No. 3;
Matches 68; Conservative 35; Mismatches 108; Indels 104; Gaps 15;

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Qy       5 RCWPR--------------VVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLS 49

Db      88 RCWFRRMMALHHGVTLDVNGTVGGAAAHWRLSFVNESAAGSGA------------ENLT 134

Qy      50 CRVKNSTCLDDSWIHPKNLTPSSPKNIYINLSV-SSTQH---------GELVPVLHVEWT 99

Db     135 CEIRAARFLSCAW----REGPAAPADVRYSLRVLNSTGHDVARCMADPGDDV----ITQC 186

Qy     100 LQTDASILYLEGAELSVLQLNTNERLCVKF-------QFLSML------------QHHRK 140

Db     187 IANDLSLL---GSEAYLVVTGRSGAGPVRFLDDVVATKALERLGPPRDVTASCNSSHCTV 243

Qy     141 RW--------------RFSFSHFVVDPGQE------YEVTVHHLPKPIPDGDPNHKSKII 180

Db     244 SWAPPSTWASLTARDFQFEVQWQSAEPGSTPRKVLVVEETRLAFPSPAPHG--GHKVKV- 300

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240

Db     301 ---RAGDTRMK-------HWGEWSPAHPLEAEDT---RVPGALLYAVTACAVLLCALALG 347

Qy     241 ENHSCFDVVKQIFAP 255

Db     348 VTCRRFEVTRRLFPP 362
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RESULT 11
G86300
hypothetical protein AAG10824.1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

```
C;Accession: G86300
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: G86300
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-682 <STO>
A;Cross-references: GB:AE005172; NID:g9989061; PIDN:AAG10824.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1


  Query Match             5.2%;  Score 92;  DB 2;  Length 682;
  Best Local Similarity   22.9%;  Pred. No. 9.1;
  Matches   71;  Conservative   36;  Mismatches  109;  Indels   94;  Gaps   17;

Qy      66 KNLTPS------SPKNIYINLSVSSTQHGE--LVPVLHVEWTLQ---------------- 101
           |:||||      :  :||:   : : :||    | ||:    |:
Db     269 KSLTPSAIWMHTTSLSIYVKKKLQALRHGNGAAVCVLYGSENLELSSHKSGPTVTFNLKR 328

Qy     102 TDASIL-YLEG---AELSVLQLNTNERLC----------------VKFQFLSMLQHHRKR 141
            | |   |||    | || :||     :|                | | ::|  :  :|
Db     329 PDGSWFGYLEVEKLASLSGIQLRAG-HICWDDNDVINGKPTGAVRVSFGYMSTFEDAKKF 387

Qy     142 WRFSFSHFVVDPGQEYEVTV--HHLPKPIPDGD-------PNHKSKIIFV---PDCEDSK 189
           |  | |   | :    ||      |: :|  |        |:|  | | |     |
Db     388 IDFIISSFASPPKKTGNGTVVSGRFPQ-LPSEDLESKESFPSHYLKSITVYPIKSCAGFS 446

Qy     190 MKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSD-------SEN 242
           :    |  :| | |    |: |  :       |  :  |   |:::| |         |:
Db     447 VIRWPLC-RTGLLHDREWMVQGLTGE------ILTQKKVPEMSLIKTFIDLEEGLLSVES 499

Qy     243 HSCFD-----VVKQIFAPRQEEFHQRANVT------------FTLSKFHWCCHHHVQVQP 285
           | |     :    : || :||   ||:             || :    |     ::
Db     500 SRCEDKLHIRIKSDSYNPRNDEFDSHANILENRNEETRINRWFTNAIGRQC-----KLLR 554

Qy     286 FFSSCLNDCL 295
           : ||   |||
Db     555 YSSSTSKDCL 564


RESULT  12
T39553
vacuolar protein sorting-associated protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39553
R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21863
A;Accession: T39553
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3131 <PUR>
A;Cross-references: EMBL:AL021767; PIDN:CAA16910.1; GSPDB:GN00067; SPDB:SPBC16C6.02c
A;Experimental source: strain 972h-; cosmid c16C6
C;Genetics:
A;Gene: SPDB:SPBC16C6.02c
A;Map position: 2
A;Introns: 8/1; 45/3; 96/3; 2958/3


  Query Match             5.2%;  Score 91.5;  DB 2;  Length 3131;
  Best Local Similarity   20.6%;  Pred. No. 68;
  Matches   68;  Conservative   54;  Mismatches  125;  Indels   83;  Gaps   15;

Qy      17 GWLLLLLNVLAPGRASP----------RLLDF----PAPVCAQEGLSCRVKNSTCLDDSW 62
           |:: | |  | | |  |          :::|:     :|:   : |:|   :::   :
Db    1898 GYVPLDLACLYPLRIRPVSKLGFLWSNQIVDWHSLNKSPL---QYLTCESTSTSWKHNLL 1954

Qy      63 IHPKNLTPSSPKNIY--------------------INLSV----------SSTQHGELVP 92
           :  :||   | :| |                    ||| :          ||   |: :|
Db    1955 VFARNLMDGSLQNDYPFLQLNILPTLQIENLLPYEINLRIIERSSGNDWRSSLSPGDSLP 2014

Qy      93 VLHV------------EWTLQ-TDASILYL---EGAELSVLQLNTNE------RLCVKF 129
           :||             :  ||  |  |:|    | ::    | |        :| :|:
Db    2015 ILHTDSKSFLLMGINVPDLDLQPVDLPIIYTPISSGQDVQTSALLTASDKQDVVKLILKY 2074

Qy     130 QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTV-----HHLPKPIPDGDPNHKSKIIFVPD 184
           : |   : |    :  :|:   :  : |    : :   || |  ::  |  |
Db    2075 EKLPGTNYVSK--VMIYPPYVIFNHTDLSIQVTSSSPNSIRYTIPSGSYSNDIKPYFYSF 2132

Qy     185 CEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
           |  :       : :|: |  :|  :|| :   :|:    |||     | |   | ||:
Db    2133 DESGRKNRAMISIDNGTSWSADIGFDTLGSSS-QVEVRKTNES---DVCLLGMSISESSG 2188

Qy     245 CFDVVKQI-FAPRQEEFHQRANVTFTLSKF 273
           | : | : | ||   |    : | :| :|
Db    2189 KFCLTKSVTFTPR-FVFKNHLDCTVSLREF 2217


RESULT  13
T26891
hypothetical protein Y44A6C.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26891
R;Ainscough, R.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z20281
A;Accession: T26891
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-333 <WIL>
A;Cross-references: EMBL:AL021489; PIDN:CAA16370.1; GSPDB:GN00023; CESP:Y44A6C.2
A;Experimental source: clone Y44A6C
C;Genetics:
A;Gene: CESP:Y44A6C.2
A;Map position: 5
A;Introns: 6/2; 155/3


  Query Match             5.2%;  Score 91;  DB 2;  Length 333;
  Best Local Similarity   20.2%;  Pred. No. 4.5;
  Matches   59;  Conservative   44;  Mismatches  105;  Indels   84;  Gaps   13;

Qy      50 CRVKNSTCLD---------DSWIHP----KNLTPSSPKNIYINLSVSSTQHGELVPVLHV 96
           | |  :| ||          |||        | |:: :   :   :       :  :| :
Db      50 CDVSENTSLDYRSNHQQLLKSWISSTEKIAQLFPTTLRTFQVTPPM-------IAAILDL 102

Qy      97 EWTLQTDASILYLEG---AELSVLQLNTNERLCVKFQFL-------SMLQHHRKRWRFSF 146
           |  :    :| ::    ||:   | : :       ||:         :: || : :  |
Db     103 ETAIPKTCDVLIIQNYVPAEMDRYQESVD-------QFMEKCHIREGVVLHH-EVYTNSP 154

Qy     147 SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFV--PDCEDSKMKMTTSCVSSGS--- 201
             | :|      ::| |    :|      ::||:::   |  || |      : |||
Db     155 KMFQLD-----YLSVTHSDWMVPSDLEEMENKIVYLDKSDFYDSDMNQFLRELKSGSSHS 209

Qy     202 -------------LWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFD 247
                        |||:  :| |: :       |||::   |     | ::|:   |
Db     210 RLQILSIQGNSWQNYWDPSDVLEGLNAE-------LWNQTERNQ---HYFLNAEHRKNFK 259

Qy     248 VVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAV 299
           :   | | ||:             |     | | :   |    ||  | :|
Db     260 KIADHFYPDQED------------GFGAELEHGVDLSEAFDFLKNDGTRVSV 299
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```
RESULT  14
T08180
PF20 protein, microtubule-associated - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T08180
R;Smith, E.; Lefebvre, P.
submitted to the EMBL Data Library, November 1996
A;Description: The PF20 gene product contains WD repeats and localizes to the inter-micr
A;Reference number: Z16400
A;Accession: T08180
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-606 <SMI>
A;Cross-references: EMBL:U78547; NID:g1813637; PID:g1813638
C;Genetics:
A;Gene: PF20
C;Keywords: microtubule


  Query Match             5.1%;  Score 89.5;  DB 2;  Length 606;
  Best Local Similarity   20.2%;  Pred. No. 13;
  Matches   61;  Conservative   34;  Mismatches  118;  Indels   89;  Gaps   13;

Qy      10 VVPGPALGWLLLLLNVLAPGRASPRL-LDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNL 68
           |  ||  ||     :: || | :|   |:|||       |:   |         :   ||
Db     283 VSAGPRSGW----ASLNAPPRRNPYADLEFPAAPVKMLSLNKTFKGHL------LSVANL 332

Qy      69 TPSSPKNIYINLSVSST------QHGELVPV--LHVEWTLQTD----ASILYLEGAELSV 116
             | | :  |   |        |:|:     | :|    |     : |   | : :|
Db     333 ALHPTKPILVTASDDKTWKMWHMPGGDLIMCGEGHKDWVAGVDFHPAGTCLASGGGDSAV 392

Qy     117 LQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHK 176
              :  :: ||     :   | :  |   |               ||| : :  |  :|
Db     393 KIWDFEKQRCV----TTFTDHKQAIWSVRF--------------HHLGEVVASGSLDHT 433

Qy     177 SKIIFVPDCEDSKMKM----------------------TTSCVSSGSLWDP--------- 205
           ::  :|     | :|                      | |   : |:||
Db     434 VRLWDLP---AGKCRMALRGHVDSVNDLAWQPFSSSLATASSDKTVSVWDARAGLCTQTY 490

Qy     206 --------NITVETLDTQHLRVD----FTLWNESTPYQV-LLESFSDSENHSCFDVVKQI 252
                  ::   | ||    |      ||:     :|  : :     |  ||||   |:
Db     491 YGHQNSCNGVSFNILGTQLASTDADGVVKLWDTRMTAEVATINTGKHPANKSCFDRSGQV 550

Qy     253 FA 254
           |
Db     551 LA 552


RESULT  15
S42841
T16G12.1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000
C;Accession: S42841
R;Thomas, K.
submitted to the EMBL Data Library, February 1994
A;Reference number: S42837
A;Accession: S42841
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-885 <THO>
A;Cross-references: EMBL:Z30317
C;Genetics:
A;Introns: 49/3; 79/2; 188/1; 205/2; 273/3; 338/1; 432/3; 515/3; 585/1; 616/3; 733/2; 77
C;Superfamily: membrane alanyl aminopeptidase


  Query Match             5.1%;  Score 89.5;  DB 2;  Length 885;
  Best Local Similarity   21.2%;  Pred. No. 20;
  Matches   65;  Conservative   44;  Mismatches  108;  Indels   89;  Gaps   15;

Qy      28 PGRASPRLLDFP----------------------APVCAQEGLSCRVKNSTCLDDSWIHP 65
           || | | : | |                      |   |||||           |::
Db     450 PGVAKPVISDTPPVFGIEPYYKGSALLNLLNNVLTPAVFQEGLS----------SYLTQ 498

Qy      66 KNLTPSSPKNIYINLSVSSTQH------GELVPVLHV--EWTLQTDASILYLEGAELSVL 117
                :||:|:: :|:|:: :|      |: : |      :|||| |: |     | :
Db     499 YGYVNASPRNLWTSLTVAAQRHNITDWNGQPLDVSSFMDPYTLQTSYPIITLTLRGTSTV 558

Qy     118 QLNTNERLCVKFQFLSMLQHHRKRWR----------FSFSHFVVDPGQEYEVTVHHLPKP 167
           |   |:: |:  : |          |             |: ||   |      :    :|
Db     559 Q--ANQQSCMSDETL---------WNVPLFTQTPGALDFNWFVNFTGGNDATWL----RP 603

Qy     168 IPDG-----------DPNHKSKIIFVPDCE-DSKMKMTTSCVSSGSLWDPNITVETLDT 214
           :| |             |:  |  :    :  | |   :|   :  | | |   ::
Db     604 LPTGYRVDNAGSTSFARINYDDKSWYSIQAQLLSNMNTMSSTTRAMLLDDANFFYQSGRW 663

Qy     215 QHLR-VDFTLW--NEST--PYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFT 269
           :  : :| ||:  || :  |::  :| |::  |   |    :|   |         |
Db     664 EMTKFLDLTLYLVNEDSLAPWEQAIEFFTEMLNR--FQYQPEIDTVRNYVIQITKN---A 718

Qy     270 LSKFHW 275
           :||| |
Db     719 VSKFQW 724


Search completed: July 17, 2001, 11:19:56
Job time: 150 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:15:41 ; Search time 34.56 Seconds
(without alignments)
564.842 Million cell updates/sec

Title: US-09-488-728-2_COPY_1_322
Perfect score: 1766
Sequence: 1 MAIRRCWPRVVPGPALGWLL.....CPVISNTTVPKPVADYIPLW 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601:*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
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21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1766	100.0	330	21	AAY97255	Soluble IL-17R/Fla
2	1766	100.0	330	21	AAY97258	Soluble IL-17R/Fla
3	1766	100.0	864	17	AAW04184	Murine interleukin
4	1766	100.0	864	19	AAW61271	Mouse interleukin-
5	1766	100.0	864	20	AAW92408	Murine IL-17R prot
6	1766	100.0	864	21	AAY99935	Murine IL-17R prot
7	1766	100.0	864	21	AAY97130	Murine interleukin
8	1766	100.0	864	21	AAY97180	Murine interleukin
9	1766	100.0	864	21	AAB03806	Murine interleukin
10	1766	100.0	864	22	AAB62060	Murine IL-17R poly
11	1766	100.0	864	22	AAY72748	Murine Interleukin
12	1254	71.0	866	17	AAW04185	Human interleukin-
13	1254	71.0	866	19	AAW61272	Human interleukin-
14	1254	71.0	866	20	AAW92409	Human IL-17R prote
15	1254	71.0	866	21	AAY99941	Human IL-17R prote
16	1254	71.0	866	21	AAY97131	Human interleukin-
17	1254	71.0	866	21	AAY97181	Human interleukin-
18	1254	71.0	866	21	AAB03807	Human interleukin-
19	1254	71.0	866	22	AAB62066	Human IL-17R (hCTL
20	1254	71.0	866	22	AAY72754	Human Interleukin-
21	282.5	16.0	426	21	AAB18750	A human interleuki
22	282.5	16.0	426	21	AAY70591	Interleukin 17-lik
23	282.5	16.0	426	21	AAY49946	Human interleukin
24	282.5	16.0	433	21	AAB18754	A human interleuki
25	282.5	16.0	433	21	AAY70595	Interleukin 17-lik
26	282.5	16.0	502	22	AAB87604	Human PRO5801. Ho
27	208.5	11.8	385	21	AAB25795	Human secreted pro
28	208.5	11.8	385	22	AAB75381	Human secreted pro
29	137	7.8	34	20	AAY39426	Human interleukin-
30	97	5.5	880	16	AAR77846	Mouse Rse rPTK. M
31	95.5	5.4	977	22	AAB31164	Amino acid sequenc
32	92	5.2	729	21	AAY44857	Mouse taste cell s
33	88	5.0	874	15	AAR60545	Murine development
34	88	5.0	874	19	AAW79145	Receptor protein t
35	88	5.0	874	20	AAW81402	Receptor protein t
36	88	5.0	993	6	AAP50116	Sequence of Hepati
37	86.5	4.9	377	16	AAR84740	Interleukin-1-beta
38	86.5	4.9	377	17	AAR88750	Human Tx protease,
39	86.5	4.9	377	17	AAW00213	Human Ich-2 protei
40	86.5	4.9	377	17	AAR90702	Interleukin-1-beta
41	86.5	4.9	377	20	AAY21718	Amino acid sequenc
42	86	4.9	322	20	AAY14072	Human BS247 specif
43	84.5	4.8	340	21	AAB03643	Rat IgE heavy chai
44	84.5	4.8	565	16	AAR76700	EIET enterotoxin e
45	84	4.8	452	17	AAR97299	Human GABA-A recep

ALIGNMENTS

RESULT 1
AAY97255
ID AAY97255 standard; peptide; 330 AA.
XX
AC AAY97255;
XX
DT 04-DEC-2000 (first entry)
XX
DE Soluble IL-17R/Flag fusion protein.
XX
KW IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW anti-asthmatic; Flag epitope; fusion protein.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Protein 1..322
FT /label= Soluble_IL-17_receptor
FT Peptide 1..31
FT /label= Signal_peptide
FT Protein 32..322
FT /label= IL-17_receptor_extracellular_domain
FT Peptide 323..330
FT /label= Flag_epitope
XX
PN US6096305-A.
XX
PD 01-AUG-2000.
XX
PF 11-FEB-1998; 98US-0022253.
XX
PR 21-MAR-1996; 96US-0620694.
PR 23-MAR-1995; 95US-0410535.

```
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-523862/47.
XX
PT   Suppressing rejection of a grafted syngeneic or allogeneic organ or
PT   tissue in a graft recipient for organ transplantation involves
PT   transfecting the organ or tissue with DNA encoding soluble
PT   interleukin-17R receptor
XX
PS   Example 3; Column -; 27pp; English.
XX
CC   A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC   cDNA library from T cell thymoma EL4 cells, which were identified as
CC   binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC   region and soluble IL-17 (CTLA-8) protein or a homologous
CC   Herpesvirus saimiri (HSV) protein, designated HSV13. Suppressing
CC   rejection of a grafted syngeneic or allogeneic organ or tissue in a
CC   graft recipient involves transfecting the organ or tissue to be
CC   transplanted with DNA encoding soluble IL-17R, so that expression of
CC   IL-17R by the engrafted organ or tissue results in suppression of
CC   rejection. Soluble IL-17R fragments comprise residues 1-322 of the murine
CC   IL-17R, residues 1-320 of the human IL-17R, and fragments of the
CC   extracellular domain that bind IL-17. The method is useful for regulating
CC   an immunoresponse, for suppressing rejection of grafted organs or tissues
CC   in the recipient and for treating or preventing diseases like allergy,
CC   asthma and autoimmune diseases.
CC   Note: This sequence does not appear in the specification. It was created
CC   from the full length murine IL-17R (see AAY97180) and the flag peptide
CC   (see AAY97183)
XX
SQ   Sequence   330 AA;


  Query Match             100.0%;  Score 1766;  DB 21;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           ||||||||||||||||||||||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT   2
AAY97258
ID   AAY97258 standard; peptide; 330 AA.
XX
AC   AAY97258;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Soluble IL-17R/Flag fusion protein.
XX
KW   IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW   HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW   anti-asthmatic; Flag epitope; fusion protein.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..322
FT                   /label= Soluble_IL-17_receptor
FT   Peptide         1..31
FT                   /label= Signal_peptide
FT   Protein         32..322
FT                   /label= IL-17_receptor_extracellular_domain
FT   Peptide         323..330
FT                   /label= Flag_epitope
XX
PN   US6100235-A.
XX
PD   08-AUG-2000.
XX
PF   11-FEB-1998;   98US-0022260.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-548298/50.
XX
PT   Regulating, treating or preventing immune or inflammatory response in a
PT   mammal, especially organ or graft rejection, allergy or asthma,
PT   comprises administering interleukin-17 receptors
XX
PS   Example 3; Column -; 27pp; English.
XX
CC   A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC   cDNA library from T cell thymoma EL4 cells, which were identified as
CC   binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC   region and soluble IL-17 (CTLA-8) protein or a homologous
CC   Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an
CC   immune or inflammatory response in a mammal comprises administering
CC   soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the
CC   murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the
CC   extracellular domain that bind IL-17. The method is useful for
CC   regulating an immunoresponse, for treating or preventing diseases like
CC   allergy, asthma and autoimmune diseases, and for suppressing rejection of
CC   grafted organs or tissues in the recipient.
CC   Note: This sequence does not appear in the specification. It was created
CC   from the full length murine IL-17R (see AAY97130) and the flag peptide
CC   (see AAY97132)
XX
SQ   Sequence   330 AA;


  Query Match             100.0%;  Score 1766;  DB 21;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy    181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy    241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy    301 VPCPVISNTTVPKPVADYIPLW 322
          ||||||||||||||||||||||
Db    301 vpcpvisnttvpkpvadyiplw 322


RESULT   3
AAW04184
ID   AAW04184 standard; Protein; 864 AA.
XX
AC   AAW04184;
XX
DT   05-DEC-1996  (first entry)
XX
DE   Murine interleukin-17 receptor.
XX
KW   Interleukin-17 receptor; IL-17R; autoimmune disease; allergy;
KW   asthma; graft rejection; inflammation; cytokine; therapy.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= Sig_peptide
FT   Domain          32..322
FT                   /label= Extracellular_domain
FT   Domain          323..343
FT                   /label= Transmembrane_domain
FT   Domain          344..864
FT                   /label= Cytoplasmic_tail
XX
PN   WO9629408-A1.
XX
PD   26-SEP-1996.
XX
PF   21-MAR-1996;   96WO-US04018.
XX
PR   07-AUG-1995;   95US-0538765.
PR   23-MAR-1995;   95US-0410535.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 1996-443184/44.
DR   N-PSDB; AAT33800.
XX
PT   DNA encoding interleukin-17 receptor - useful for regulating immune
PT   and inflammatory responses, or to suppress graft rejection
XX
PS   Claim 1; Page 29-32; 52pp; English.
XX
CC   The murine interleukin-17 receptor (IL-17R) (AAW04184) is a type I
CC   transmembrane protein that binds IL-17 (CTLA-8, see also AAW02386)
CC   and HVS13 (AAW02387), a viral homologue of IL-17.  Its amino acid
CC   sequence was deduced from a cDNA clone (AAT33800) isolated from murine
CC   thymoma EL4 cells.  Soluble, recombinant forms of the receptor
CC   (partic. amino acids 1-322) can be prepd. in transformed host cells
CC   and used to regulate immune and inflammatory responses, in methods
CC   for suppressing rejection of grafted organs or tissue, and in
CC   assays of IL-17 and IL-17R.
XX
SQ   Sequence   864 AA;
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  Query Match           100.0%;  Score 1766;  DB 17;  Length 864;
  Best Local Similarity  100.0%;  Pred. No. 8.6e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy     61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy    121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy    181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy    241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy    301 VPCPVISNTTVPKPVADYIPLW 322
          ||||||||||||||||||||||
Db    301 vpcpvisnttvpkpvadyiplw 322


RESULT   4
AAW61271
ID   AAW61271 standard; Protein; 864 AA.
XX
AC   AAW61271;
XX
DT   12-OCT-1998  (first entry)
XX
DE   Mouse interleukin-17 receptor.
XX
KW   Interleukin-17 receptor; IL-17 receptor; mouse; nitric oxide;
KW   cartilage; osteoarthritis; autoimmune disease; inflammation;
KW   therapy.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= Sig_peptide
FT   Protein         32..864
FT                   /label= Mat_protein
FT   Protein         1..322
FT                   /label= Soluble_IL-17R
FT                   /note= "Claim 2(a)"
FT   Domain          32..322
FT                   /label= Extracellular
FT   Domain          323..343
FT                   /label= Transmembrane
FT   Domain          344..864
FT                   /label= Extracellular
XX
PN   WO9823284-A1.
XX
PD   04-JUN-1998.
XX
PF   21-NOV-1997;   97WO-US21451.
XX
PR   27-NOV-1996;   96US-0052525.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Troutt AB;
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XX
DR   WPI; 1998-322457/28.
DR   N-PSDB; AAV27591.
XX
PT   Reducing nitric oxide production by cartilage associated cells - by
PT   contacting cells with soluble interleukin-17 receptor, useful to
PT   treat osteoarthritis and autoimmune and inflammatory diseases
XX
PS   Claim 2(a); Page 20-23; 41pp; English.
XX
CC   This polypeptide comprises mouse full-length interleukin-17
CC   receptor (IL-17R).  A claimed method for reducing the amount of
CC   nitric oxide produced by a cartilage associated cell comprises
CC   contacting the cell with a soluble IL-17R, especially claimed
CC   soluble murine or human (see AAW61272) IL-17R comprising the signal
CC   peptide and extracellular domains of the respective full-length
CC   receptors.  Recombinant soluble IL-17R polypeptides can be obtained
CC   using prokaryotic or eukaryotic (for glycosylated products)
CC   expression systems.  A cDNA sequence (see AAV27591) coding for
CC   full-length murine IL-17R is provided.  IL-17 is known to stimulate
CC   nitric oxide production from cartilage-associated cells in
CC   individuals with osteoarthritis.  Inhibitors of nitric oxide
CC   production, such as soluble IL-17R, may therefore be useful to
CC   ameliorate the effects of nitric oxide in osteoarthritis as well
CC   as in other disease conditions in which nitric oxide plays a role,
CC   e.g. autoimmune and inflammatory diseases.
XX
SQ   Sequence   864 AA;


  Query Match             100.0%;  Score 1766;  DB 19;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           |||||||||||||||||||||||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT   5
AAW92408
ID   AAW92408 standard; Protein; 864 AA.
XX
AC   AAW92408;
XX
DT   21-APR-1999  (first entry)
XX
DE   Murine IL-17R protein.
XX
KW   IL-17R; murine; interleukin-17 receptor; immunoregulator; inhibitor;
KW   T cell proliferation; T cell activation; organ; graft; rejection;
KW   autoimmune disease; allergy; asthma; treatment; inflammatory disease;
KW   B cell proliferation; immunoglobulin secretion; immunogen.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= signal_peptide
FT   Protein         32..864
XX
PN   US5869286-A.
XX
PD   09-FEB-1999.
XX
PF   21-MAR-1996;   96US-0620694.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 1999-152766/13.
DR   N-PSDB; AAX01921.
XX
PT   Isolated interleukin-17 receptor DNA - used to develop products for
PT   treating e.g. organ or graft rejection, autoimmune disease, allergy,
PT   asthma or inflammatory disease
XX
PS   Disclosure; Column 25-30; 25pp; English.
XX
CC   This sequence represents a murine interleukin-17 receptor (IL-17R).
CC   IL-17R polypeptides have immunoregulatory activity. They can be used for
CC   inhibiting T cell proliferation, or for inhibiting T cell activation. In
CC   particular they can be used for preventing or treating organ or graft
CC   rejection, autoimmune disease, allergy or asthma. They can also be used
CC   for the prevention or treatment of inflammatory disease in which
CC   activated T cells play a role or for inhibiting B cell proliferation
CC   or immunoglobulin secretion. The IL-17 polypeptides can also be used
CC   as immunogens, reagents in in vitro assays, or as binding agents for
CC   affinity purification procedures.
XX
SQ   Sequence   864 AA;


  Query Match             100.0%;  Score 1766;  DB 20;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           |||||||||||||||||||||||
Db     301 vpcpvisnttvpkpvadyiplw 322
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RESULT   6
AAY99935
ID   AAY99935 standard; Protein; 864 AA.
XX
AC   AAY99935;
XX
DT   10-JAN-2001  (first entry)
XX
DE   Murine IL-17R protein.
XX
KW   IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
KW   murine; antibody; immune suppression.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= Signal_peptide
FT   Domain          32..322
FT                   /label= Extracellular_domain
FT   Domain          323..353
FT                   /label= Transmembrane_domain
FT   Domain          354..864
FT                   /label= Cytoplasmic_domain
FT   Protein         32..864
FT                   /label= IL-17R
XX
PN   US6072037-A.
XX
PD   06-JUN-2000.
XX
PF   12-FEB-1998;   98US-0022696.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-411206/35.
DR   N-PSDB; AAA61238.
XX
PT   Antibodies immunoreactive with interleukin-17 receptor protein useful
PT   in interfering with receptor binding to CTLA-8, as components of
PT   diagnostic or research assays or in affinity purification of the
PT   receptor -
XX
PS   Claim 1; Column 25-30; 25pp; English.
XX
CC   The present invention relates to a novel receptor that binds Interleukin
CC   17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC   HVS13. The receptor is a type I transmembrane protein which is referred
CC   to as IL-17R. Murine thymona EL4 cells were found to express a
CC   receptor for IL-17. An EL4 mammalian expression library was screened
CC   and a cDNA encoding the receptor was identified. The present sequence
CC   is the murine IL-7R protein. The cDNA was used to isolate DNA encoding
CC   human IL-17R by cross species hybridisation. The human IL-17R cDNA and
CC   protein are described in AAA61240 and AAY99941. Soluble forms of the
CC   receptor may be used to regulate immune responses, for example to
CC   suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC   amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be useful
CC   as components of diagnostic or research assays. Such antibodies may also
CC   be used in affinity purification of the receptor.
XX
SQ   Sequence   864 AA;


 Query Match             100.0%;  Score 1766;  DB 21;  Length 864;
 Best Local Similarity   100.0%;  Pred. No. 8.6e-169;
 Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           ||||||||||||||||||||||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT   7
AAY97130
ID   AAY97130 standard; Protein; 864 AA.
XX
AC   AAY97130;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Murine interleukin-17 receptor.
XX
KW   IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW   HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW   anti-asthmatic.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..322
FT                   /label= Soluble_IL-17_receptor
FT   Peptide         1..31
FT                   /label= Signal_peptide
FT   Protein         32..864
FT                   /label=  Mature_protein
FT   Domain          32..322
FT                   /label= Extracellular_domain
FT   Domain          323..343
FT                   /label= Transmembrane_domain
FT   Domain          344..864
FT                   /label= Cytoplasmic_tail
XX
PN   US6100235-A.
XX
PD   08-AUG-2000.
XX
PF   11-FEB-1998;   98US-0022260.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-548298/50.
DR   N-PSDB; AAA51987.
XX
```

```
PT   Regulating, treating or preventing immune or inflammatory response in a
PT   mammal, especially organ or graft rejection, allergy or asthma,
PT   comprises administering interleukin-17 receptors
XX
PS   Claim 1; Column 25-30; 26pp; English.
XX
CC   A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC   cDNA library from T cell thymoma EL4 cells, which were identified as
CC   binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC   region and soluble IL-17 (CTLA-8) protein or a homologous
CC   Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an
CC   immune or inflammatory response in a mammal comprises administering
CC   soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the
CC   murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the
CC   extracellular domain that bind IL-17. The method is useful for regulating
CC   an immunoresponse, for treating or preventing diseases like allergy,
CC   asthma and autoimmune diseases, and for suppressing rejection of grafted
CC   organs or tissues in the recipient.
XX
SQ   Sequence   864 AA;


  Query Match             100.0%;  Score 1766;  DB 21;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           ||||||||||||||||||||||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT   8
AAY97180
ID   AAY97180 standard; Protein; 864 AA.
XX
AC   AAY97180;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Murine interleukin-17 receptor.
XX
KW   IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW   HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW   anti-asthmatic.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..322
FT                   /label= Soluble_IL-17_receptor
FT   Peptide         1..31
FT                   /label= Signal_peptide
FT   Protein         32..864
FT                   /label=  Mature_protein
FT   Domain          32..322
FT                   /label= Extracellular_domain
FT   Domain          323..343
FT                   /label= Transmembrane_domain
FT   Domain          344..864
FT                   /label= Cytoplasmic_tail
XX
PN   US6096305-A.
XX
PD   01-AUG-2000.
XX
PF   11-FEB-1998;   98US-0022253.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-523862/47.
DR   N-PSDB; AAA52145.
XX
PT   Suppressing rejection of a grafted syngeneic or allogeneic organ or
PT   tissue in a graft recipient for organ transplantation involves
PT   transfecting the organ or tissue with DNA encoding soluble
PT   interleukin-17R receptor
XX
PS   Claim 1; Column 25-30; 27pp; English.
XX
CC   A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC   cDNA library from T cell thymoma EL4 cells, which were identified as
CC   binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC   region and soluble IL-17 (CTLA-8) protein or a homologous
CC   Herpesvirus saimiri (HSV) protein, designated HSV13. Suppressing
CC   rejection of a grafted syngeneic or allogeneic organ or tissue in a graft
CC   recipient involves transfecting the organ or tissue to be transplanted
CC   with DNA encoding soluble IL-17R, so that expression of IL-17R by the
CC   engrafted organ or tissue results in suppression of rejection. Soluble
CC   IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues
CC   1-320 of the human IL-17R, and fragments of the extracellular domain
CC   that bind IL-17. The method is useful for regulating an immunoresponse,
CC   for suppressing rejection of grafted organs or tissues in the recipient
CC   and for treating or preventing diseases like allergy, asthma and
CC   autoimmune diseases.
XX
SQ   Sequence   864 AA;


  Query Match             100.0%;  Score 1766;  DB 21;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy    301 VPCPVISNTTVPKPVADYIPLW 322
          |||||||||||||||||||||||
Db    301 vpcpvisnttvpkpvadyiplw 322


RESULT   9
AAB03806
ID   AAB03806 standard; Protein; 864 AA.
XX
AC   AAB03806;
XX
DT   13-OCT-2000  (first entry)
XX
DE   Murine interleukin-17 (IL-17) receptor protein sequence.
XX
KW   Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; antiallergic;
KW   immunosuppressive; organ rejection; graft rejection; autoimmune disease;
KW   allergy; asthma; mouse.
XX
OS   Mus sp.
XX
PN   US6072033-A.
XX
PD   06-JUN-2000.
XX
PF   11-FEB-1998;   98US-0022255.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 2000-411205/35.
DR   N-PSDB; AAA59870.
XX
PT   Interleukin-17 receptor protein useful for regulating immune functions
PT   and for preventing or treating organ or graft rejection, autoimmune
PT   disease, allergy or asthma in human  -
XX
PS   Claim 1; Column 25-30; 26pp; English.
XX
CC   This invention relates to an isolated and purified interleukin-17
CC   receptor (IL-17R). A soluble IL-17 protein (CTLA8) and a herpesvirus
CC   siamiri (HVS13) open reading frame (homologous to CTLA8) were expressed
CC   as fusion proteins comprising an immunoglobulin Fc region, and used to
CC   screen for the expression of the IL-17R. The screening identified the
CC   novel receptor of the invention. IL-17R is a type I transmembrane
CC   protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic
CC   and antiallergic activities, and is an inhibitor of T cell proliferation
CC   and activation. IL-17R can be used to regulate immune functions, and is
CC   useful for preventing or treating organ or graft rejection, autoimmune
CC   disease, allergy or asthma. The present sequence represents the murine
CC   interleukin-17 receptor amino acid sequence identified in the invention.
XX
SQ   Sequence   864 AA;


  Query Match             100.0%;  Score 1766;  DB 21;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mairrcwprvvpgpalgwllllnvlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy     61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy    121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy    181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy    241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy    301 VPCPVISNTTVPKPVADYIPLW 322
          |||||||||||||||||||||||
Db    301 vpcpvisnttvpkpvadyiplw 322


RESULT  10
AAB62060
ID   AAB62060 standard; Protein; 864 AA.
XX
AC   AAB62060;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Murine IL-17R polypeptide.
XX
KW   CTLA-8; interleukin-17; IL-17; IL-17 receptor; IL-17R; mouse;
KW   immunosuppressive; antiallergic; antiasthmatic; antiinflammatory.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /note= "signal peptide"
FT   Protein         32..864
FT                   /note= "mature protein"
FT   Domain          32..322
FT                   /note= "extracellular domain"
FT   Domain          323..343
FT                   /note= "transmembrane domain"
FT   Domain          344..864
FT                   /note= "cytoplasmic domain"
XX
PN   US6197525-B1.
XX
PD   06-MAR-2001.
XX
PF   11-FEB-1998;   98US-0022257.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Yao Z,  Spriggs MK,  Fanslow WC;
XX
DR   WPI; 2001-234480/24.
DR   N-PSDB; AAF57186.
XX
PT   New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors
PT   and (antagonists or mimetics of) the interaction between IL-17 and
PT   IL-17 receptor, useful for treating autoimmune diseases -
XX
PS   Claim 1; Columns 19-26; 26pp; English.
XX
CC   The invention is directed towards assays for detection of interleukin-17
CC   (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the
CC   interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R
CC   protein and a detecting reagent. The method is useful for inhibiting
CC   binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also
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CC   useful for preventing or treating organ or graft rejection, autoimmune
CC   diseases, allergy, asthma and inflammatory diseases in which activated
CC   T-cells play an important role. The present sequence represents a
CC   mouse IL-17R polypeptide.
XX
SQ   Sequence   864 AA;


  Query Match             100.0%;  Score 1766;  DB 22;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-169;
  Matches  322;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mairrcwprvvpgpalgwllllln vlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           |||||||||||||||||||||||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT  11
AAY72748
ID   AAY72748 standard; Protein; 864 AA.
XX
AC   AAY72748;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Murine Interleukin-17 receptor (IL-17R) or CTLA-8 receptor.
XX
KW   Murine; Interleukin-17 receptor; IL-17R; immunosuppressive; antiallergic;
KW   antiasthmatic; antiinflammatory; graft rejection; autoimmune disease;
KW   inflammatory disease; allergy; CTLA-8; immunogen; asthma.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= Signal_peptide
FT   Protein         32..864
FT                   /label= Mature_murine_IL-17_receptor
FT   Domain          32..322
FT                   /label= Extracellular_domain
FT   Domain          323..343
FT                   /label= Transmembrane_domain
FT   Domain          344..864
FT                   /label= Cytoplasmic_tail
XX
PN   US6191104-B1.
XX
PD   20-FEB-2001.
XX
PF   11-FEB-1998;   98US-0022259.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Spriggs MK,  Fanslow WC;
XX
DR   WPI; 2001-217901/22.
DR   N-PSDB; AAD02813.
XX
PT   Suppressing rejection of grafted organ or tissue in graft recipient,
PT   involves administering to recipient a composition comprising
PT   interleukin 17 receptor protein -
XX
PS   Claim 1; Column 25-30; 26pp; English.
XX
CC   The present sequence is murine Interleukin-17 receptor (IL-17R) or
CC   CTLA-8 receptor.
CC   The invention relates to Interleukin-17 receptors (IL-17R),
CC   Interleukin-17 and their corresponding nucleic acid molecules. IL-17R is
CC   a Type I transmembrane protein which is used for regulating the immune
CC   response. The invention is useful for suppressing rejection of a grafted
CC   organ or tissue in a graft recipient. Soluble IL-17 (CTLA-8) receptors
CC   are useful for preventing or treating organ or graft rejection,
CC   autoimmune disease, allergy, asthma, and inflammatory disease in which
CC   activated T-cells play a role. Soluble IL-17 fusion proteins are used to
CC   screen cells for the expression of IL-17 receptor. Derivatives of IL-17R
CC   are also used as immunogens, reagents in in vitro assays, or as binding
CC   agents for affinity purification procedures.
XX
SQ   Sequence   864 AA;


  Query Match             100.0%;  Score 1766;  DB 22;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-169;
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Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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Db       1 mairrcwprvvpgpalgwllllln vlapgrasprlldfpapvcaqeglscrvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           |||||||||||||||||||||||
Db     301 vpcpvisnttvpkpvadyiplw 322


RESULT  12
AAW04185
ID   AAW04185 standard; Protein; 866 AA.
XX
AC   AAW04185;
XX
DT   05-DEC-1996  (first entry)
XX
DE   Human interleukin-17 receptor.
XX
KW   Interleukin-17 receptor; IL-17R; autoimmune disease; allergy;
KW   asthma; graft rejection; inflammation; cytokine; therapy.
```

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Sig_peptide
FT   Domain          28..320
FT                   /label= Extracellular_domain
FT   Domain          321..341
FT                   /label= Transmembrane_domain
FT   Domain          342..866
FT                   /label= Cytoplasmic_tail
XX
PN   WO9629408-A1.
XX
PD   26-SEP-1996.
XX
PF   21-MAR-1996;   96WO-US04018.
XX
PR   07-AUG-1995;   95US-0538765.
PR   23-MAR-1995;   95US-0410535.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 1996-443184/44.
DR   N-PSDB; AAT33801.
XX
PT   DNA encoding interleukin-17 receptor - useful for regulating immune
PT   and inflammatory responses, or to suppress graft rejection
XX
PS   Claim 1; Page 41-44; 52pp; English.
XX
CC   The human interleukin-17 receptor (IL-17R) (AAW04184) is a type I
CC   transmembrane protein.  Its amino acid sequence was deduced from
CC   a cDNA clone (AAT33801) isolated from a human peripheral blood
CC   lymphocyte library.  Soluble, recombinant forms of the receptor
CC   (partic. amino acids 1-320) can be prepd. in transformed host cells
CC   and used to regulate immune and inflammatory responses, in methods
CC   for suppressing rejection of grafted organs or tissue, and in
CC   assays of IL-17 and IL-17R.
XX
SQ   Sequence   866 AA;


  Query Match             71.0%;  Score 1254;  DB 17;  Length 866;
  Best Local Similarity   71.4%;  Pred. No. 2.8e-117;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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Db       1 mgaarsppsavpgpllgllllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           |||||:||||||||:: | |  : || |:| || |:|||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           |||||||:|:||| |:|| :||||:|||||||| |||||||||||||||||||:||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
            ||||| ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||: :  | ||| |||||:||| ||     || | ||:||||||||||||: |
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           | || : :|  |:|: ||:|||
Db     301 vscpempdt--pepipdymplw 320
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RESULT  13
AAW61272
ID   AAW61272 standard; Protein; 866 AA.
XX
AC   AAW61272;
XX
DT   12-OCT-1998  (first entry)
XX
DE   Human interleukin-17 receptor.
XX
KW   Interleukin-17 receptor; IL-17 receptor; human; nitric oxide;
KW   cartilage; osteoarthritis; autoimmune disease; inflammation;
KW   therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Sig_peptide
FT   Protein         28..866
FT                   /label= Mat_protein
FT   Protein         1..320
FT                   /label= Soluble_IL-17R
FT                   /note= "Claim 2(b)"
FT   Domain          28..320
FT                   /label= Extracellular
FT   Domain          321..341
FT                   /label= Transmembrane
FT   Domain          342..866
FT                   /label= Extracellular
XX
PN   WO9823284-A1.
XX
PD   04-JUN-1998.
XX
PF   21-NOV-1997;   97WO-US21451.
XX
PR   27-NOV-1996;   96US-0052525.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Troutt AB;
XX
DR   WPI; 1998-322457/28.
DR   N-PSDB; AAV27592.
XX
PT   Reducing nitric oxide production by cartilage associated cells - by
PT   contacting cells with soluble interleukin-17 receptor, useful to
PT   treat osteoarthritis and autoimmune and inflammatory diseases
XX
PS   Claim 2(b); Page 27-31; 41pp; English.
XX
CC   This polypeptide comprises human full-length interleukin-17
CC   receptor (IL-17R).  A claimed method for reducing the amount of
CC   nitric oxide produced by a cartilage associated cell comprises
CC   contacting the cell with a soluble IL-17R, especially claimed
CC   soluble human or mouse (see AAW61271) IL-17R comprising the signal
CC   peptide and extracellular domains of the respective full-length
CC   receptors.  Recombinant soluble IL-17R polypeptides can be obtained
CC   using prokaryotic or eukaryotic (for glycosylated products)
CC   expression systems.  A cDNA sequence coding for full-length human
CC   IL-17R is provided (see AAV27592).  IL-17 is known to stimulate
CC   nitric oxide production from cartilage-associated cells in
CC   individuals with osteoarthritis.  Inhibitors of nitric oxide
CC   production, such as soluble IL-17R, may therefore be useful to
CC   ameliorate the effects of nitric oxide in osteoarthritis as well as
CC   in other disease conditions in which nitric oxide plays a role,
CC   e.g. autoimmune and inflammatory diseases.
XX
SQ   Sequence   866 AA;
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```
  Query Match             71.0%;  Score 1254;  DB 19;  Length 866;
  Best Local Similarity   71.4%;  Pred. No. 2.8e-117;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

Qy       1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           |||||:||||||||:: | |  : || |:| || |:|||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||:||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           |||||| ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           |||||||: :  | ||| |||||:||| ||     || | ||:|||||||||||||: |
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           | || : :|  |:|: ||:|||
Db     301 vscpempdt--pepipdymplw 320


RESULT  14
AAW92409
ID   AAW92409 standard; Protein; 866 AA.
XX
AC   AAW92409;
XX
DT   21-APR-1999  (first entry)
XX
DE   Human IL-17R protein.
XX
KW   IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor;
KW   T cell proliferation; T cell activation; organ; graft; rejection;
KW   autoimmune disease; allergy; asthma; treatment; inflammatory disease;
KW   B cell proliferation; immunoglobulin secretion; immunogen.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= signal_peptide
FT   Protein         28..866
FT                   /label= IL-17R
XX
PN   US5869286-A.
XX
PD   09-FEB-1999.
XX
PF   21-MAR-1996;   96US-0620694.
XX
PR   21-MAR-1996;   96US-0620694.
PR   23-MAR-1995;   95US-0410535.
PR   07-AUG-1995;   95US-0538765.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Fanslow WC,  Spriggs MK,  Yao Z;
XX
DR   WPI; 1999-152766/13.
DR   N-PSDB; AAX01922.
XX
PT   Isolated interleukin-17 receptor DNA - used to develop products for
PT   treating e.g. organ or graft rejection, autoimmune disease, allergy,
PT   asthma or inflammatory disease
XX
PS   Disclosure; Column 43-48; 25pp; English.
XX
CC   This sequence represents a human interleukin-17 receptor (IL-17R).
CC   IL-17R polypeptides have immunoregulatory activity. They can be used for
CC   inhibiting T cell proliferation, or for inhibiting T cell activation. In
CC   particular they can be used for preventing or treating organ or graft
CC   rejection, autoimmune disease, allergy or asthma. They can also be used
CC   for the prevention or treatment of inflammatory disease in which
CC   activated T cells play a role or for inhibiting B cell proliferation
CC   or immunoglobulin secretion. The IL-17 polypeptides can also be used
CC   as immunogens, reagents in in vitro assays, or as binding agents for
CC   affinity purification procedures.
XX
SQ   Sequence   866 AA;


  Query Match             71.0%;  Score 1254;  DB 20;  Length 866;
  Best Local Similarity   71.4%;  Pred. No. 2.8e-117;
  Matches  230;  Conservative   30;  Mismatches   60;  Indels    2;  Gaps    1;

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Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           |||||:||||||||:: | |  : || |:| || |:|||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||:||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
           |||||| ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           |||||| :  | ||| |||||:||| ||     || | ||:|||||||||||||: |
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           | || : :|  |:|: ||:|||
Db     301 vscpempdt--pepipdymplw 320


RESULT  15
AAY99941
ID   AAY99941 standard; Protein; 866 AA.
XX
AC   AAY99941;
XX
DT   10-JAN-2001  (first entry)
XX
DE   Human IL-17R protein.
XX
KW   IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
KW   murine; antibody; immune suppression.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Signal_peptide
FT   Domain          28..320
FT                   /label= Extracellular_domain
FT   Domain          321..341
FT                   /label= Transmembrane_domain
FT   Domain          342..866
FT                   /label= Cytoplasmic_domain
FT   Protein         32..866
FT                   /label= IL-17R
XX
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PN US6072037-A.
XX
PD 06-JUN-2000.
XX
PF 12-FEB-1998; 98US-0022696.
XX
PR 21-MAR-1996; 96US-0620694.
PR 23-MAR-1995; 95US-0410535.
PR 07-AUG-1995; 95US-0538765.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Fanslow WC, Spriggs MK, Yao Z;
XX
DR WPI; 2000-411206/35.
DR N-PSDB; AAA61240.
XX
PT Antibodies immunoreactive with interleukin-17 receptor protein useful
PT in interfering with receptor binding to CTLA-8, as components of
PT diagnostic or research assays or in affinity purification of the
PT receptor -
XX
PS Claim 1; Column 43-48; 25pp; English.
XX
CC The present invention relates to a novel receptor that binds Interleukin
CC 17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC HVS13. The receptor is a type I transmembrane protein which is referred
CC to as IL-17R. Murine thymona EL4 cells were found to express a
CC receptor for IL-17. An EL4 mammalian expression library was screened
CC and a cDNA encoding the receptor was identified. The murine IL-17R cDNA
CC and protein are described in AAA61238 and AAY99935. The cDNA was used to
CC isolate DNA encoding human IL-17R by cross species hybridisation. The
CC present sequence is the human IL-7R protein. Soluble forms of the
CC receptor may be used to regulate immune responses, for example to
CC suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be
CC useful as components of diagnostic or research assays. Such antibodies
CC may also be used in affinity purification of the receptor.
XX
SQ Sequence 866 AA;

Query Match 71.0%; Score 1254; DB 21; Length 866;
Best Local Similarity 71.4%; Pred. No. 2.8e-117;
Matches 230; Conservative 30; Mismatches 60; Indels 2; Gaps 1;

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           |   |  |  |||| || ||||| ||||| || ||||  | ||:| ||:| |||||||||
Db       1 mgaarsppsavpgpllglllllgvlapggaslrlldhralvcsqpglnctvknstcldd 60

Qy      61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
           |||||:||||||||:: | |  : || |:| || |:||||||||||||||||||||||||
Db      61 swihprnltpsspkdlqiqlhfahtqqgdlfpvahiewtlqtdasilylegaelsvlqln 120

Qy     121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
           |||||||:|:||| |:|| :||||:|||||||| ||||||||||||||||||||:||
Db     121 tnerlcvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf 180

Qy     181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
            ||||| ::||:|| |:|||||||||||||||:   ||| |||||||| ||:|| ||
Db     181 lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm 240

Qy     241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
           ||||||: :  | ||| ||||||:||| ||     || | ||:||||||||||||||: |
Db     241 enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300

Qy     301 VPCPVISNTTVPKPVADYIPLW 322
           | || : :|  |:|: ||:|||
Db     301 vscpempdt--pepipdymplw 320
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Job time: 193 sec

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